

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 3, 2004, 11:55:12 ; Search time 76 Seconds

(without alignments)  
1531.705 Million cell updates/sec

Title: US-09-876-252-130

Perfect score: 2156

Sequence: 1 MGSPNGSGDGEAREPWP.....DTGGDTGVTGTTTSANVKTMG 412

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_23Jan04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2156	100.0	412	3 AAB02854	Aab02854 Human G p
2	2149	99.7	412	3 AAY54145	Aay54145 Amino aci
3	2149	99.7	412	4 AAB68478	Aab68478 Amino aci
4	2149	99.7	412	4 AAB62652	Aab62652 Long form
5	2149	99.7	412	5 ABG30936	Abg30936 Human G p
6	2149	99.7	412	6 AAB81933	Abp81933 Human mot
7	2149	99.7	501	4 AAB65822	Abp65822 Human GPR
8	2135	99.0	412	5 AAB09535	Abb09535 Human mot
9	1741	80.8	400	4 AAB68477	Aab68477 Amino aci
10	1575	73.1	386	3 AAY54146	Aay54146 Amino aci
11	1575	73.1	386	4 AAB62653	Aab62653 Short for
12	1143.5	53.0	271	4 AAB68476	Aab68476 Amino aci
13	901	41.8	363	3 AAY54147	Aay54147 The pufie
14	864.5	40.1	363	4 AAB68479	Aab68479 Amino aci
15	864.5	40.1	366	7 AAY90666	Aay90666 Human mut
16	864.5	40.1	366	7 ADC22729	Adc22729 Human G p
17	859.5	39.9	349	3 AAY69293	Aay69293 A canine
18	857.5	39.8	366	3 AAY70345	Aay70345 Human G p
19	857.5	39.8	366	3 AAY90632	Aay90632 Human G p
20	857.5	39.8	366	4 AAB97376	Aab97376 Rat growt
21	857.5	39.8	366	4 AAB62650	Aab62650 Human G-p
22	857.5	39.8	366	5 ABB09534	Abb09534 Human ghr
23	857.5	39.8	366	7 ADC22607	Adc22607 Human G p
24	857.5	39.8	366	8 ADD35398	Add35398 Human gro
25	857	39.7	353	2 AAW19215	Aaw19215 Swine gro

26	857	39.7	353	2 AAW19608	Aaw19608 Pig growt
27	855.5	39.7	364	3 AAY54565	Aay54565 A mouse g
28	855.5	39.7	364	4 AAB97377	Aab97377 Rat growt
29	854	39.6	361	2 AAW19217	Aaw19217 Human gro
30	854	39.6	362	2 AAW19610	Aaw19610 Human gro
31	851.5	39.5	364	2 AAW19613	Aaw19613 Rat growt
32	839.5	38.9	364	2 AAW19220	Aaw19220 Rat growt
33	668.5	31.0	271	2 AAW19219	Aaw19219 Human gro
34	668.5	31.0	271	2 AAW19612	Aaw19612 Human gro
35	638.5	29.6	289	2 AAW19611	Aaw19611 Human gro
36	638.5	29.6	289	2 AAB81828	Abb81828 Human gro
37	635	29.5	289	2 AAW19216	Aaw19216 Swine gro
38	635	29.5	289	2 AAW19609	Aaw19609 Pig growt
39	633.5	29.4	289	2 AAW19218	Aaw19218 Human gro
40	498	23.1	418	4 ABB56371	Abb56371 Non-endog
41	495	23.0	418	2 AAB98562	Aar98562 Human neu
42	491	22.8	418	6 AAB81861	Abb81861 Human neu
43	491	22.8	542	4 ABG12316	Abg12316 Novel hum
44	490.5	22.8	403	3 AAY90673	Aay90673 Human mut
45	490.5	22.8	403	5 ABB95171	Abb95171 Human GPC

## ALIGNMENTS

### RESULT 1

AAB02854

ID AAB02854 standard; protein; 412 AA.

XX AC AAB02854;

XX DT 22-AUG-2000 (first entry)

XX DE Human G protein coupled receptor hGPR38

XX KW Human; G protein coupled receptor; GPCR; transmembrane receptor;

XX KW identification; agonist; screening; therapeutic; pharmaceutical; mutant.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200022131-A2.

XX PD 20-APR-2000.

XX PF 13-OCT-1999; 99WO-US024065.

XX PR 13-OCT-1998; 98US-00170496.

XX PR 12-NOV-1998; 98US-0108029P.

XX PR 20-NOV-1998; 98US-0109213P.

XX PR 27-NOV-1998; 98US-0110060P.

XX PR 16-FEB-1999; 99US-0120416P.

XX PR 26-FEB-1999; 99US-0121852P.

XX PR 12-MAR-1999; 99US-0123944P.

XX PR 12-MAR-1999; 99US-0123945P.

XX PR 12-MAR-1999; 99US-0123946P.

XX PR 12-MAR-1999; 99US-0123948P.

XX PR 12-MAR-1999; 99US-0123949P.

XX PR 12-MAR-1999; 99US-0123951P.

XX PR 28-MAY-1999; 99US-0136436P.

XX PR 28-MAY-1999; 99US-0136437P.

XX PR 28-MAY-1999; 99US-0136439P.

XX PR 28-MAY-1999; 99US-0137127P.

XX PR 28-MAY-1999; 99US-0137131P.

XX PR 28-MAY-1999; 99US-0137567P.

XX PR 29-JUN-1999; 99US-0141448P.

XX PR 27-AUG-1999; 99US-0151114P.

XX PR 03-SEP-1999; 99US-0152524P.

XX PR 29-SEP-1999; 99US-0156555P.

XX PR 29-SEP-1999; 99US-0156633P.

XX PR 29-SEP-1999; 99US-0156634P.

XX PR 29-SEP-1999; 99US-0156653P.

XX PR 01-OCT-1999; 99US-0157280P.

PR 01-OCT-1999; 99US-0157281P.  
 PR 01-OCT-1999; 99US-0157282P.  
 PR 01-OCT-1999; 99US-0157283P.  
 PR 01-OCT-1999; 99US-0157294P.  
 PR 12-OCT-1999; 99US-00416760.  
 PR 12-OCT-1999; 99US-00417044.  
 XX (AREN-) ARENA PHARM INC.  
 PA Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;  
 PI Gore M, Liaw CW, Lin I, Lowitz K, White C;  
 XX WPI; 2000-317986/27.  
 DR N-PSDB; AAA46116.  
 XX Non-endogenous, human G protein-coupled receptors for screening receptor,  
 PT inverse or partial agonists useful as therapeutic agents.  
 XX Example 2; Page 168-169; 187pp; English.  
 XX The present invention describes transmembrane receptors, preferably human  
 CC G protein coupled receptors (GPCR), for which the endogenous ligand is  
 CC unknown (orphan GPCR receptors). More specifically the present invention  
 CC relates to non-endogenous, constitutively activated versions of a human  
 CC GPCR. These non-endogenous human GPCRs can be useful for the direct  
 CC identification of candidate compounds as receptors agonists, inverse  
 CC agonists or partial agonists for use as pharmaceutical agents. AAA46017  
 CC to AAA46126 and AAB02825 to AAB02859 represent sequences used in the  
 CC exemplification of the present invention  
 XX Sequence 412 AA;

Query Match 100.0%; Score 2156; DB 3; Length 412;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-194;  
 Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGSPWNGSDGPEGAREPPWALPCDERRCSPFFLGALVPVTAVALCLFVVGVSGNVTV 60  
 DB 1 MGSPWNGSDGPEGAREPPWALPCDERRCSPFFLGALVPVTAVALCLFVVGVSGNVTV 60  
 QY 61 MLIGRYDMRTTNLYLGSMAVSDLLILLGLPFDLYRLWRSRPVFGPFLCLRLSLYVGE 120  
 DB 61 MLIGRYDMRTTNLYLGSMAVSDLLILLGLPFDLYRLWRSRPVFGPFLCLRLSLYVGE 120  
 QY 121 CTYATLLHMTALSVERYLAI CRPLARVLVTRRRVRLIAVLMAVALLSAGPFLVGE 180  
 DB 121 CTYATLLHMTALSVERYLAI CRPLARVLVTRRRVRLIAVLMAVALLSAGPFLVGE 180  
 QY 181 QDPGISVVGNGTARIASSPLASSPPLWLSRAPPPSPGPEAAALFSRECRPSA 240  
 DB 181 QDPGISVVGNGTARIASSPLASSPPLWLSRAPPPSPGPEAAALFSRECRPSA 240  
 QY 241 QLGAIRVLMVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRERGHQTKRVL 300  
 DB 241 QLGAIRVLMVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRERGHQTKRVL 300  
 QY 301 LVVLAFTICWLPFHVGRIIINTEDSRWYFSQYFNIVALQLFVLSASINPILYNLISK 360  
 DB 301 LVVLAFTICWLPFHVGRIIINTEDSRWYFSQYFNIVALQLFVLSASINPILYNLISK 360  
 QY 361 KYRAAFAKLLARKSRPRGFRHSRDTAGEVAGDTGGDTVGVTSTSANVKTWG 412  
 DB 361 KYRAAFAKLLARKSRPRGFRHSRDTAGEVAGDTGGDTVGVTSTSANVKTWG 412

RESULT 2  
 ID AAY54145  
 XX AAY54145 standard; protein; 412 AA.  
 AC AAY54145;

XX 27-MAR-2000 (first entry)  
 DT  
 XX

DE Amino acid sequence of the motilin receptor splice variant MTL-R1A.  
 XX Motilin receptor; G-protein coupled receptor; MTL-R1; GPR38;  
 KW spliced form; MTL-R1A; MTL-R1B; Gastric motility disorder;  
 KW functional defect; neurological disorder; scleroderma; colonoscopy;  
 KW paraneoplastic syndrome; radiation induced dysmotility; diabetes;  
 KW infection; stress-related motility disorder; psychogenic disorder;  
 KW gastroparesis; gastro-oesophageal reflux disease; constipation;  
 KW chronic idiopathic pseudo obstruction; acute faecal impaction;  
 KW postoperative ileus; gallstones; infantile colic; diarrhoea;  
 KW irritable bowel syndrome; non-ulcer dyspepsion; non-cardiac chest pain;  
 KW endoscopy; duodenal intubation.  
 XX Homo sapiens.  
 OS  
 XX WO9964436-A1.  
 FN  
 XX 16-DEC-1999.  
 PD  
 XX 08-JUN-1999; 99WO-US012773.  
 PF  
 XX 12-JUN-1998; 98US-0089098P.  
 PR  
 XX (MERI ) MERCK & CO INC.  
 PA  
 XX Feighner SD, Patchett AA, Tan C, McKee K, Macneil D, Howard AD;  
 PI Pong S, Smith RG;  
 PI WPI; 2000-105868/09.  
 DR N-PSDB; AAZ45403.  
 DR  
 XX Novel receptor protein for screening compounds used in treating irritable  
 PT bowel syndrome, constipation and other gastric conditions.  
 XX Claim 3; Fig 3; 44pp; English.

The present sequence represents splice variant MTL-R1A of the motilin  
 CC receptor. The gene encodes a G-protein coupled receptor, and is  
 CC designated MTL-R1 (also GPR38). Two spliced forms of GPR38 exist, MTL-R1A  
 CC (see AAY54145) and MTL-R1B (see AAY54146). MTL-R1A is a functional seven  
 CC transmembrane domain form, and MTL-R1B is a truncated five transmembrane  
 CC domain. The MTL-R1 proteins are used to identify agonists and antagonists  
 CC which can be used for treating gastric motility disorders, functional  
 CC defects, disorders secondary to neurological disorders e.g. scleroderma,  
 CC paraneoplastic syndromes radiation induced dysmotility, diabetes,  
 CC infections, stress-related motility disorders, psychogenic disorders,  
 CC gastroparesis, gastro-oesophageal reflux disease, constipation, chronic  
 CC idiopathic pseudo obstruction, acute faecal impaction, postoperative  
 CC ileus, gallstones, infantile colic, irritable bowel syndrome, non-ulcer  
 CC dyspepsion, non-cardiac chest pain and diarrhoea. They can also be used  
 CC in the preparation for colonoscopy, endoscopy and duodenal intubation  
 XX Sequence 412 AA;  
 QY Query Match 99.7%; Score 2149; DB 3; Length 412;  
 DB Best Local Similarity 99.8%; Pred. No. 8.4e-194;  
 QY Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 DB 1 MGSPWNGSDGPEGAREPPWALPCDERRCSPFFLGALVPVTAVALCLFVVGVSGNVTV 60  
 DB 1 MGSPWNGSDGPEGAREPPWALPCDERRCSPFFLGALVPVTAVALCLFVVGVSGNVTV 60  
 QY 61 MLIGRYDMRTTNLYLGSMAVSDLLILLGLPFDLYRLWRSRPVFGPFLCLRLSLYVGE 120  
 DB 61 MLIGRYDMRTTNLYLGSMAVSDLLILLGLPFDLYRLWRSRPVFGPFLCLRLSLYVGE 120  
 QY 121 CTYATLLHMTALSVERYLAI CRPLARVLVTRRRVRLIAVLMAVALLSAGPFLVGE 180  
 DB 121 CTYATLLHMTALSVERYLAI CRPLARVLVTRRRVRLIAVLMAVALLSAGPFLVGE 180  
 QY 181 QDPGISVVGNGTARIASSPPLASSPPLWLSRAPPPSPGPEAAALFSRECRPSA 240  
 DB 181 QDPGISVVGNGTARIASSPPLASSPPLWLSRAPPPSPGPEAAALFSRECRPSA 240

QY 241 QLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHROTQVRL 300  
DB 241 QLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHROTQVRL 300  
QY 301 LVVVLAFIICWLPFHVGRIIYINTEDSRMVFYSQYFNIVALQLFYLSASINPILYNLISK 360  
DB 301 LVVVLAFIICWLPFHVGRIIYINTEDSRMVFYSQYFNIVALQLFYLSASINPILYNLISK 360  
QY 361 KYRAAFKLLARKSRPRGFHRSRDTAGEVAGDTGGDTGVYTETTSANVKTMG 412  
DB 361 KYRAAFKLLARKSRPRGFHRSRDTAGEVAGDTGGDTGVYTETTSANVKTMG 412

RESULT 3  
AAB68478  
ID AAB68478 standard; protein; 412 AA.  
XX  
AC AAB68478;  
XX  
DT 23-JUL-2001 (first entry)  
XX  
DE Amino acid sequence of a human motilin receptor polypeptide.  
XX  
KW Motilin receptor; gastrointestinal disease; gastric motility disorder;  
KW Gastroparesis; irritable bowel syndrome; diarrhoea.  
XX  
OS Homo sapiens.  
XX  
PN WO200132710-A1.  
XX  
PD 10-MAY-2001.  
XX  
PF 25-OCT-2000; 2000WO-US029426.  
XX  
PR 29-OCT-1999; 99US-0162264P.  
XX  
PA (MERL ) MERCK & CO INC.  
XX  
PI Tan C, McKee K;  
XX  
DR WPI; 2001-343479/36.  
DR N-PSDB; AAF85449.  
XX  
PT Novel polypeptides related to dog and rabbit motilin receptor  
PT polypeptide, comprising unique regions from dog and motilin receptor  
PT amino acid sequence, useful for identifying compounds for treating  
PT diarrhea in humans.  
XX  
PS Disclosure; Page 32-33; 42pp; English.  
XX  
CC The present sequence represents a human motilin receptor polypeptide. The  
CC specification describes an unique sequence present in exon 1 of the dog  
CC motilin receptor, which is not present in human or Sphaeroides nephelus  
CC 75E7 motilin receptor sequences. The unique nucleic acid sequence is  
CC useful for measuring the ability of a compound to affect motilin receptor  
CC activity. Motilin receptor polynucleotides and polypeptides are used to  
CC identify therapeutic compounds which are useful for treating  
CC gastrointestinal diseases and disorders such as gastric motility  
CC disorders, gastroparesis, irritable bowel syndrome, and diarrhoea  
XX  
SQ Sequence 412 AA;

Query Match 99.7%; Score 2149; DB 4; Length 412;  
Best Local Similarity 99.8%; Pred. No. 8.4e-194;  
Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGEGAREPPWALPPCDERRCSPPFLGALVPVAVCI-CLFVVGSGNVVTV 60  
DB 1 MGSPWNGSDGEGAREPPWALPPCDERRCSPPFLGALVPVAVCI-CLFVVGSGNVVTV 60  
QY 61 MLIGRYDRMTTNNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPFLCRLSLYVGE 120

DB 61 MLIGRYDRMTTNNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPFLCRLSLYVGE 120  
QY 121 CTYATLHMTALSVERYLAI CRPLRARVLVTRRRVRLIAVLWVALLSAGPFLPLVGVE 180  
DB 121 CTYATLHMTALSVERYLAI CRPLRARVLVTRRRVRLIAVLWVALLSAGPFLPLVGVE 180  
QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPSGPETAFAALFSRECRPSPA 240  
DB 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPSGPETAFAALFSRECRPSPA 240  
QY 241 QLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHROTQVRL 300  
DB 241 QLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHROTQVRL 300  
QY 301 LVVVLAFIICWLPFHVGRIIYINTEDSRMVFYSQYFNIVALQLFYLSASINPILYNLISK 360  
DB 301 LVVVLAFIICWLPFHVGRIIYINTEDSRMVFYSQYFNIVALQLFYLSASINPILYNLISK 360  
QY 361 KYRAAFKLLARKSRPRGFHRSRDTAGEVAGDTGGDTGVYTETTSANVKTMG 412  
DB 361 KYRAAFKLLARKSRPRGFHRSRDTAGEVAGDTGGDTGVYTETTSANVKTMG 412

RESULT 4  
AAB62652  
ID AAB62652 standard; protein; 412 AA.  
XX  
AC AAB62652;  
XX  
DT 23-JUL-2001 (first entry)  
XX  
DE Long form of motilin receptor, GPR-38A isoform.  
XX  
KW zsig33; signal transduction; hormone; enzyme; neural development;  
KW gastric contractility; nutrient uptake; digestive; pancreatic; human;  
KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;  
KW glucose; osteopathic; anorectic; vulnery; immunomodulator; GHS-R;  
KW G-protein coupled receptor; motilin receptor; GPR38; GPR-38A; isoform.  
XX  
OS Homo sapiens.  
XX  
PN WO200138355-A2.  
XX  
PD 31-MAY-2001.  
XX  
PF 22-NOV-2000; 2000WO-US032074.  
XX  
PR 22-NOV-1999; 99US-0166765P.  
XX  
PA (ZYMO ) ZYMOGENETICS INC.  
XX  
PI Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;  
XX  
DR WPI; 2001-355879/37.  
DR N-PSDB; AAF83683.  
XX  
PT Forming reversible peptide receptor complex for purifying cell and  
PT peptides, stimulating signal transduction and modulating hormone  
PT secretion, involves contacting a receptor with zsig33 polypeptide.  
XX  
PS Disclosure; Page 102-104; 111pp; English.  
XX  
CC The invention relates to a method of forming a reversible peptide-  
CC receptor complex that involves providing an immobilized receptor, and  
CC contacting the receptor with a zsig33 peptide (comprising residues 24-37  
CC of AAB62649), where the receptor binds to the zsig33 peptide. The method  
CC is useful for purifying cells, purifying a peptide, stimulating signal  
CC transduction in a cell expressing a receptor. It is also useful for  
CC modulating secretion of hormones, neural development and/or utilization,  
CC gastric contractility, nutrient uptake, secretion of digestive and  
CC pancreatic enzymes and hormones, secretion of insulin-like growth factor  
CC -I, secretion of non-zsig33 proteins. It is useful for modulating growth  
CC hormone secretion in a mammal having a disease associated with abnormal

CC levels of growth hormone, such as osteoporosis, bone repair, bone remodeling, low osteoblast levels, cartilage repair and remodeling, CC skeletal dysplasia, immune suppression, obesity, growth retardation, protein catabolic responses after surgery, cachexia, protein loss, CC dwarfism, wound healing and ovulation induction, treating a mammal having CC a metabolic disorder requiring neurological feedback, such as satiety CC regulation, glucose absorption and metabolism and neuropathy-associated CC gastrointestinal disorders, and stimulating glucose-induced insulin CC release in a mammal. The present sequence represents the long form of CC motilin receptor, GPR-38A (one of the two isoforms of GPR38 which result CC from alternative splicing). GPR38 has homology to the human G-protein CC coupled receptor, GHS-R

XX  
SQ Sequence 412 AA;

Query Match 99.7%; Score 2149; DB 4; Length 412;  
Best Local Similarity 99.8%; Pred. No. 8.4e-194;  
Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGSPWNGSDGEGAREPPWPALPPCDERRCSPFPLGALVPVTAVCLCLFVVGSGNVTV 60  
Db 1 MGSPWNGSDGEGAREPPWPALPPCDERRCSPFPLGALVPVTAVCLCLFVVGSGNVTV 60

Qy 61 MLIGRYDMRTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPFLCRLSLYVGE 120  
Db 61 MLIGRYDMRTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPFLCRLSLYVGE 120

Qy 121 CTYATLLHMTALSVERYLAI CRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVGV 180  
Db 121 CTYATLLHMTALSVERYLAI CRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVGV 180

Qy 181 QDPGISVVPGLNGTARIASSPLASSPPLWLRAPPPSPGPTAEAAALFSRECRPSPA 240  
Db 181 QDPGISVVPGLNGTARIASSPLASSPPLWLRAPPPSPGPTAEAAALFSRECRPSPA 240

Qy 241 QLGLARVLMVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTQKRVL 300  
Db 241 QLGLARVLMVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTQKRVL 300

Qy 301 LVVVLAFIICWLPFHVGRIIYINTEDSRMVFSQYFNIVALQFLYLSASINPILYNLISK 360  
Db 301 LVVVLAFIICWLPFHVGRIIYINTEDSRMVFSQYFNIVALQFLYLSASINPILYNLISK 360

Qy 361 KYRAAAFLLLLARKSRPRGHRSDTAGVAGDTGGDTVGVTETSANVKTWG 412  
Db 361 KYRAAAFLLLLARKSRPRGHRSDTAGVAGDTGGDTVGVTETSANVKTWG 412

RESULT 5  
ID ABG30936  
XX ABG30936 standard; protein; 412 AA.  
AC ABG30936;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human G protein-coupled receptor 38 (GPR38).  
XX  
KW Human; G protein-coupled receptor 38; receptor; GPR38;  
KW Alzheimer's disease; Parkinson's disease; ulcerative colitis;  
KW Crohn's disease; Hodgkin's disease; glioblastoma; breast carcinoma;  
KW colon carcinoma; lung small cell carcinoma; lung adenocarcinoma;  
KW pancreatic small cell carcinoma; pancreatic adenocarcinoma.  
XX  
OS Homo sapiens.  
XX  
FH Key  
FT Region 15..31  
FT /note= "Antigenic fragment"  
FT Region 217..232  
FT /note= "Antigenic fragment"  
FT Region 276..291  
FT /note= "Antigenic fragment"  
FT

FT Region 373..388  
FT /note= "Antigenic fragment"  
XX  
FN WO200257791-A2.  
XX  
PD 25-JUL-2002.  
XX  
PF 29-NOV-2001; 2001WO-US045219.  
XX  
PR 29-NOV-2000; 2000US-0250251P.  
PR 30-NOV-2000; 2000US-0250452P.  
XX  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
XX  
FI Brown JP, Burmer GC, Roush CL, Kulander BG;  
XX  
DR WPI; 2002-566812/60.  
DR N-PSDB; ABK90132.  
XX  
PT Assay for detecting Alzheimer's disease, Parkinson's disease, ulcerative colitis, Crohn's disease, Hodgkin's disease, glioblastoma or carcinoma, comprises using a binding partner for G protein coupled receptor 38.  
PT  
XX Disclosure; Fig 2; 112pp; English.  
XX  
CC The present invention relates to a new assay method that involves contacting a binding partner specific for G protein coupled receptor (GPR) 38 with specific cells. The method of the invention is useful for the detection of an increased risk of Alzheimer's disease, Parkinson's disease, ulcerative colitis, Crohn's disease, Hodgkin's disease, glioblastoma, or carcinoma. GPR 38 is used to manufacture a medicament for inhibiting, treating or preventing Alzheimer's disease, Parkinson's disease, ulcerative colitis, Crohn's disease, Hodgkin's disease, glioblastoma, breast carcinoma, colon carcinoma, lung small cell carcinoma, lung adenocarcinoma, pancreatic small cell carcinoma, and pancreatic adenocarcinoma. An agonist or antagonist to GPR 38 are used to manufacture a medicament able to reduce the symptoms of these diseases. Nucleic acids encoding GPR 38 can also be used to treat the diseases. The present amino acid sequence represents the human G protein-coupled receptor 38 (GPR38) of the invention

XX  
SQ Sequence 412 AA;

Query Match 99.7%; Score 2149; DB 5; Length 412;  
Best Local Similarity 99.8%; Pred. No. 8.4e-194;  
Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGSPWNGSDGEGAREPPWPALPPCDERRCSPFPLGALVPVTAVCLCLFVVGSGNVTV 60  
Db 1 MGSPWNGSDGEGAREPPWPALPPCDERRCSPFPLGALVPVTAVCLCLFVVGSGNVTV 60

Qy 61 MLIGRYDMRTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPFLCRLSLYVGE 120  
Db 61 MLIGRYDMRTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPFLCRLSLYVGE 120

Qy 121 CTYATLLHMTALSVERYLAI CRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVGV 180  
Db 121 CTYATLLHMTALSVERYLAI CRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVGV 180

Qy 181 QDPGISVVPGLNGTARIASSPLASSPPLWLRAPPPSPGPTAEAAALFSRECRPSPA 240  
Db 181 QDPGISVVPGLNGTARIASSPLASSPPLWLRAPPPSPGPTAEAAALFSRECRPSPA 240

Qy 241 QLGLARVLMVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTQKRVL 300  
Db 241 QLGLARVLMVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTQKRVL 300

Qy 301 LVVVLAFIICWLPFHVGRIIYINTEDSRMVFSQYFNIVALQFLYLSASINPILYNLISK 360  
Db 301 LVVVLAFIICWLPFHVGRIIYINTEDSRMVFSQYFNIVALQFLYLSASINPILYNLISK 360

Qy 361 KYRAAAFLLLLARKSRPRGHRSDTAGVAGDTGGDTVGVTETSANVKTWG 412  
Db 361 KYRAAAFLLLLARKSRPRGHRSDTAGVAGDTGGDTVGVTETSANVKTWG 412

Db 361 KYRAAFKLLARKSRPGFHRSDTAGEVAGDTGDTVGYTETSANVKTMG 412

## RESULT 6

ABP81993  
ID ABP81993 standard; protein; 412 AA.

AC ABP81993;

XX 04-MAR-2003 (first entry)

DE Human motilin receptor GPR38 protein SEQ ID NO:473.

XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
KW G protein-coupled receptor modulator; antibody; immune-related disease;  
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
KW immunological-related cell proliferative disease; autoimmune disease;  
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
KW hyperextension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
KW ulcer.

XX Homo sapiens.

XX WO200261087-A2.

XX 08-AUG-2002.

XX 19-DEC-2001; 2001WO-US050107.

XX 19-DEC-2000; 2000US-0257144P.

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

XX Burmer GC, Roush CL, Brown JP;

XX WPT; 2003-046718/04.

XX N-PSDB; ABZ42842.

XX New isolated antigenic peptides e.g., for G protein-coupled receptors  
PT (GPCR), useful for diagnosing and designing drugs for treating conditions  
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
PT autoimmune diseases.

XX Disclosure; Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising: (a)  
XX any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
XX acids. Also described: (1) an assay for the detection of a particular G  
XX protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
XX and (2) an isolated antibody having high specificity and high affinity or  
XX avidity for a particular GPCR. (I) can be used as GPCR modulators and in  
XX gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
XX antibody against a particular GPCR, and in the production of specific  
XX antibodies. The peptides and antibodies are also useful for detecting the  
XX presence or absence of corresponding GPCRs. The antigenic peptides for  
XX GPCRs and antibodies are useful for diagnosing and designing drugs for  
XX treating immune-related diseases, growth-related diseases, cell  
XX regeneration-related diseases, immunological-related cell proliferative  
XX diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
XX atherosclerosis, bacterial, fungal, protozoan or viral infections,  
XX osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
XX inflammation, allergies, Crohn's disease, diabetes, graft versus host  
XX disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
XX anxiety, depression, schizophrenia, dementia, mental retardation, memory  
XX loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
XX hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
XX any other disorder in which GPCRs are involved. The antibodies may be  
XX used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode  
XX GPCR proteins given in ABP81675 to ABP82018, which are used in the

CC exemplification of the present invention

XX Sequence 412 AA;

Query Match 99.7%; Score 2149; DB 6; Length 412;

Best Local Similarity 99.8%; Pred. No. 8.4e-194;

Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGEGAREPPWFPALPCDERRCSPFPGALVPTVAVCLCLFVVGVSGNVVTV 60

Db 1 MGSPWNGSDGEGAREPPWFPALPCDERRCSPFPGALVPTVAVCLCLFVVGVSGNVVTV 60

QY 61 MLIGRYDMETTTNLYLGSMAVSDLLILLGLPFDLYLWRSRPVFGPLLCRLSLYVGE 120

Db 61 MLIGRYDMETTTNLYLGSMAVSDLLILLGLPFDLYLWRSRPVFGPLLCRLSLYVGE 120

QY 121 CTVATLLHMTALSVERVIALCRPLARAVLTVRRVRALIAVLMAVALLSAGPFLFLVGE 180

Db 121 CTVATLLHMTALSVERVIALCRPLARAVLTVRRVRALIAVLMAVALLSAGPFLFLVGE 180

QY 181 QDQGISVVGINGTARTIASSPPLWLSRAPPPSGPETAAEAAALFSRECRSPA 240

Db 181 QDQGISVVGINGTARTIASSPPLWLSRAPPPSGPETAAEAAALFSRECRSPA 240

QY 241 QLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRPLRGPAASGRGRCHROTQVRL 300

Db 241 QLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRPLRGPAASGRGRCHROTQVRL 300

QY 301 LVVLAFLIICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQFLYLSASINPILYNLISK 360

Db 301 LVVLAFLIICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQFLYLSASINPILYNLISK 360

QY 361 KYRAAFAKLLARKSRPGFHRSDTAGEVAGDTGDTVGYTETSANVKTMG 412

Db 361 KYRAAFAKLLARKSRPGFHRSDTAGEVAGDTGDTVGYTETSANVKTMG 412

## RESULT 7

AAG65822

ID AAG65822 standard; protein; 501 AA.

XX AAG65822;

XX 30-JAN-2002 (first entry)

XX Human GPR38 variant GPR38V polypeptide.

XX GPR38V; variant; antibacterial; cytostatic; analgesic; antiasthmatic;  
XX anti-Parkinsonian; hypertensive; hypotensive; antidiabetic; osteopathic;  
XX antiallergic; antimigraine; neuroleptic; nootropic; anticonvulsant;  
XX antiulcer; antiemetic; cardiant; vaccine; human.

XX Homo sapiens.

XX WO200164836-A2.

XX 07-SEP-2001.

XX 28-FEB-2001; 2001WO-US006277.

XX 01-MAR-2000; 2000US-00516315.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

XX Elshourbagy N, Shabon U;

XX WPI; 2001-638956/73.

XX N-PSDB; AAI66989.

XX New human GPR38V polypeptide and polynucleotide, useful for treating e.g.  
XX bacterial, fungal, protozoal and viral infections, cancers or allergies,  
XX as vaccines, and for identifying agonists and antagonists potentially  
XX useful in therapy.

XX  
PS Claim 1; Page 26; 32pp; English.  
XX  
CC This represents a human GPR38 variant (GPR38V) polypeptide. GPR38V can be  
CC expressed by standard recombinant methodology. The polynucleotides and  
CC polypeptides are used in the treatment of bacterial, fungal, protozoal  
CC and viral infections, infections caused by HIV-1 or HIV-2, pain, cancers,  
CC diabetes, obesity, anorexia, asthma, Parkinson's disease, acute heart  
CC failure, hypertension, urinary retention, osteoporosis, or dyskinesias,  
CC ulcers, migraine, psychotic and neurological disorders, and allergies.  
CC They are also useful for identifying agonists and antagonists that are  
CC potentially useful in therapy, as vaccines to induce immunological  
CC response in a mammal. The polypeptides may also be used as immunogens to  
CC produce antibodies immunospecific for the polypeptides, and to identify  
CC membrane bound or soluble receptors  
XX  
SQ Sequence 501 AA;  
Query Match 99.7%; Score 2149; DB 4; Length 501;  
Best Local Similarity 99.8%; Pred. No. 1.1e-193;  
Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MGSPWNGSDGEGAREPPWPALPPCDERRCSPFPLGALVPVTAVALCLFVVGSGNVTV 60  
Db MGSPWNGSDGEGAREPPWPALPPCDERRCSPFPLGALVPVTAVALCLFVVGSGNVTV 149  
QY 61 MLIGRYDMRTTNLYLGSMVSDLLILGLPDIYRLWRSRPWVFGPLLCLSLYVGE 120  
Db MLIGRYDMRTTNLYLGSMVSDLLILGLPDIYRLWRSRPWVFGPLLCLSLYVGE 209  
QY 121 CTYATLLHMTALSVERYLAI CRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGV 180  
Db CTYATLLHMTALSVERYLAI CRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGV 269  
QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPSPGPPETAATAALFSRECRPSA 240  
Db QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPSPGPPETAATAALFSRECRPSA 329  
QY 241 QLGLRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRPPLGPAASGRGRHQTKEVL 300  
Db QLGLRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRPPLGPAASGRGRHQTKEVL 389  
QY 301 LVVLAFTICWLPFHVGRIIYINTEDSRMVFSQYFNIVALQLFYLASINPILYNLISK 360  
Db LVVLAFTICWLPFHVGRIIYINTEDSRMVFSQYFNIVALQLFYLASINPILYNLISK 449  
QY 361 KYRAAAFLLARKSRPRGFRHSDTAGVAGDTGGDTVGVTETTSANVKTMG 412  
Db KYRAAAFLLARKSRPRGFRHSDTAGVAGDTGGDTVGVTETTSANVKTMG 501  
RESULT 8  
ABB09535  
ID ABB09535 standard; protein; 412 AA.  
XX  
AC ABB09535;  
XX  
DT 22-OCT-2002 (first entry)  
XX  
DE Human motilin receptor.  
XX  
KW Human; motilin receptor; appetite; food intake; agonist; analogue;  
KW undernutrition; anorexia; cachexia; malignant disease; infection;  
KW inflammatory disease; weight loss; antagonist; obesity; anorectic;  
KW anabolic; ghrelin receptor homologue; receptor.  
XX  
OS Homo sapiens.  
XX  
FN WO200260472-A1.  
XX  
PD 08-AUG-2002.  
XX  
PF 31-JAN-2002; 2002WO-JP000765.

XX  
PR 31-JAN-2001; 2001JP-00024423.  
XX  
PA (CHUS ) CHUGAI SEIYAKU KK.  
XX  
PI Inui A, Asakawa A, Kaga T;  
XX  
XX WPI; 2002-619206/66.  
XX  
PT Remedies for diseases with hypo-nutrition status e.g. inappetence and  
PT cachexia, containing ghrelin or its analogs including agonists and  
PT antagonists.  
XX  
PS Disclosure; Fig 1B; 50pp; Japanese.  
XX  
CC The invention relates to the use of ghrelin or its analogues for the  
CC treatment of diseases associated with undernutrition such as anorexia,  
CC and also relates to the use of ghrelin antagonists for the prevention or  
CC treatment of obesity. The invention additionally discloses a method for  
CC screening ghrelin agonists or antagonists by measuring the amount of food  
CC intake, neuropeptide Y (NPY) expression, binding of NPY to NPY receptor  
CC Y1, oxygen consumption, gastric emptying, or activity of the vagus nerve.  
CC Intracerebroventricular (ICV) administration of ghrelin in animals was  
CC found to increase food intake over a period of 24 hours. Ghrelin and its  
CC analogues may therefore be used to treat conditions such as loss of  
CC appetite, anorexia, cachexia, malignant diseases, and weight loss  
CC associated with infection or inflammatory diseases. Conversely, ghrelin  
CC antagonists may be used in the treatment of obesity. The present sequence  
CC represents the human motilin receptor, a homologue of the ghrelin  
CC receptor (ABB09534) which is referred to in the disclosure of the  
CC invention  
XX  
SQ Sequence 412 AA;  
Query Match 99.0%; Score 2135; DB 5; Length 412;  
Best Local Similarity 99.3%; Pred. No. 1.8e-192;  
Matches 409; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MGSPWNGSDGEGAREPPWPALPPCDERRCSPFPLGALVPVTAVALCLFVVGSGNVTV 60  
Db 1 MGSPWNGSDGEGAREPPWPALPPCDERRCSPFPLGALVPVTAVALCLFVVGSGNVTV 60  
QY 61 MLIGRYDMRTTNLYLGSMVSDLLILGLPDIYRLWRSRPWVFGPLLCLSLYVGE 120  
Db 61 MLIGRYDMRTTNLYLGSMVSDLLILGLPDIYRLWRSRPWVFGPLLCLSLYVGE 120  
QY 121 CTYATLLHMTALSVERYLAI CRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGV 180  
Db 121 CTYATLLHMTALSVERYLAI CRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGV 180  
QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPSPGPPETAATAALFSRECRPSA 240  
Db 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPSPGPPETAATAALFSRECRPSA 240  
QY 241 QLGLRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRPPLGPAASGRGRHQTKEVL 300  
Db 241 QLGLRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRPPLGPAASGRGRHQTKEVL 300  
QY 301 LVVLAFTICWLPFHVGRIIYINTEDSRMVFSQYFNIVALQLFYLASINPILYNLISK 360  
Db 301 LVVLAFTICWLPFHVGRIIYINTEDSRMVFSQYFNIVALQLFYLASINPILYNLISK 360  
QY 361 KYRAAAFLLARKSRPRGFRHSDTAGVAGDTGGDTVGVTETTSANVKTMG 412  
Db 361 KYRAAAFLLARKSRPRGFRHSDTAGVAGDTGGDTVGVTETTSANVKTMG 412  
RESULT 9  
AAB68477  
ID AAB68477 standard; protein; 400 AA.  
XX  
AC AAB68477;  
XX

DT 23-JUL-2001 (first entry)  
 XX Amino acid sequence of a rabbit motilin receptor polypeptide.  
 KW Motilin receptor; gastrointestinal disease; gastric motility disorder;  
 KW gastroparesis; irritable bowel syndrome; diarrhoea.  
 OS Oryctolagus cuniculus.  
 XX  
 FN WO200132710-A1.  
 XX 10-MAY-2001.  
 XX 25-OCT-2000; 2000WO-US029426.  
 XX 29-OCT-1999; 99US-0162264P.  
 XX (MERI ) MERCK & CO INC.  
 XX Tan C, McKee K;  
 XX WPI; 2001-343479/36.  
 DR N-PSDB; AAF85448.  
 XX  
 XX Novel polypeptides related to dog and rabbit motilin receptor  
 PT polypeptide, comprising unique regions from dog and motilin receptor  
 PT amino acid sequence, useful for identifying compounds for treating  
 PT diarrhea in humans.  
 XX  
 XX Claim 8; Page 18; 42pp; English.  
 XX  
 XX The present sequence represents a rabbit motilin receptor polypeptide.  
 CC The specification describes a unique sequence present in exon 1 of the  
 CC dog motilin receptor, which is not present in human or Sphaeroides  
 CC nephelus 7587 motilin receptor sequences. The unique nucleic acid  
 CC sequence is useful for measuring the ability of a compound to affect  
 CC motilin receptor activity. Motilin receptor polynucleotides and  
 CC polypeptides are used to identify therapeutic compounds which are useful  
 CC for treating gastrointestinal diseases and disorders such as gastric  
 CC motility disorders, gastroparesis, irritable bowel syndrome, and  
 CC diarrhoea  
 XX  
 XX Sequence 400 AA;  
 XX  
 Query Match 80.8%; Score 1741; DB 4; Length 400;  
 Best Local Similarity 83.7%; Pred. No. 2.3e-155;  
 Matches 343; Conservative 11; Mismatches 44; Indels 12; Gaps 3;  
 QY 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPTAVCLCLFVVGSGNVVTV 60  
 DB 1 MGSPWNGSDGPEAREPPWALPPCDERRCSPFPLGTLVPTAVCLGLFAVVGSGNVTV 60  
 QY 61 MLIGRYDRMTTNLYLGSMAVSDLLILGLPDLVRLWRSPWVGPGLCLSLVYVGG 120  
 DB 61 LLIIGRYDRMTTNLYLGSMAVSDLLILGLPDLVRLWRSPWVGPGLCLSLVYVGG 120  
 QY 121 CTYATLLHMTALSVRYLAICRPLRVLVTRRRVALLAVALLSAGPFLVGV 180  
 DB 121 CTYASLLHMTALSVRYLAICRPLRVLVTRRRVALLAVALLSAGPFLVGV 180  
 QY 181 QPGISVPLGNTARIASSPLASSPPLMLSRAPPSPPGPTABAAALFSRECRPSA 240  
 DB 181 QDPAPVAAPDRNTV-----PLDPSP-----APASPPSGP-GAFAAALFSRECRPSA 228  
 QY 241 QLGALRVMLVWTAYTFPLFLCLSLIYGLIGRLWSSRPLRGPAASGRGHRQTVRL 300  
 DB 229 QUGLLRVMLVWTAYTFPLFLCLSLIYGLIARGLRGPLRGPAATGRGHRQTVRL 288  
 QY 301 LVVLAFLICWLPFFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPLYNLSK 360  
 DB 289 LVVLAFLICWLPFFHVGRIIYINTQSRMMYFSQYFNIVALQLFYLSASINPLYNLSK 348  
 QY 361 KYRAAAFKLLARKSRPRGFHRSRDTAGEVAGTGDGTGVYTETSANVKT 410

DB 349 KYRAAARLLRLRSRAGPSVCGSRGPEQDVAGDTGDTAGTETSANTKT 398  
 RESULT 10  
 AAY54146  
 ID AAY54146 standard; protein; 386 AA.  
 XX  
 AC AAY54146;  
 XX  
 DT 27-MAR-2000 (first entry)  
 XX  
 DE Amino acid sequence of the motilin receptor splice variant MTL-R1b.  
 XX  
 KW Motilin receptor; G-protein coupled receptor; MTL-R1; GPR38;  
 KW spliced form; MTL-R1a; MTL-R1b; gastric motility disorder;  
 KW functional defect; neurological disorder; scleroderma; colonoscopy;  
 KW paraneoplastic syndrome; radiation induced dysmotility; diabetes;  
 KW infection; stress-related motility disorder; psychogenic disorder;  
 KW gastroparesis; gastro-oesophageal reflux disease; constipation;  
 KW chronic idiopathic pseudo obstruction; acute faecal impaction;  
 KW postoperative ileus; gallstones; infantile colic; diarrhoea;  
 KW irritable bowel syndrome; non-ulcer dyspepsia; non-cardiac chest pain;  
 KW endoscopy; duodenal intubation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9964436-A1.  
 XX  
 XX 16-DEC-1999.  
 XX  
 XX 08-JUN-1999; 99WO-US012773.  
 XX  
 XX 12-JUN-1998; 98US-0089098P.  
 XX  
 XX (MERI ) MERCK & CO INC.  
 XX  
 XX Feighner SD, Patchett AA, Tan C, McKee K, Macneil D, Howard AD;  
 XX Pong S, Smith RG;  
 XX  
 XX WPI; 2000-105868/09.  
 XX N-PSDB; AA245404.  
 XX  
 XX Novel receptor protein for screening compounds used in treating irritable  
 XX bowel syndrome, constipation and other gastric conditions.  
 XX  
 XX Claim 5; Fig 5; 44pp; English.  
 XX  
 XX The present sequence represents splice variant MTL-R1b of the motilin  
 XX receptor. The gene encodes a G-protein coupled receptor, and is  
 XX designated MTL-R1 (also GPR38). Two spliced forms of GPR38 exist, MTL-R1A  
 XX (see AAY54145) and MTL-R1B (see AAY54146). MTL-R1A is a functional seven  
 XX transmembrane domain form, and MTL-R1B is a truncated five transmembrane  
 XX domain. The MTL-R1 proteins are used to identify agonists and antagonists  
 XX which can be used for treating gastric motility disorders, functional  
 XX defects, disorders secondary to neurological disorders e.g. scleroderma,  
 XX paraneoplastic syndromes radiation induced dysmotility, diabetes,  
 XX infections, stress-related motility disorders, psychogenic disorders,  
 XX gastroparesis, gastro-oesophageal reflux disease, constipation, chronic  
 XX idiopathic pseudo obstruction, acute faecal impaction, postoperative  
 XX ileus, gallstones, infantile colic, irritable bowel syndrome, non-ulcer  
 XX dyspepsia, non-cardiac chest pain and diarrhoea. They can also be used  
 XX in the preparation for colonoscopy, endoscopy and duodenal intubation  
 XX  
 XX Sequence 386 AA;  
 XX  
 Query Match 73.1%; Score 1575; DB 3; Length 386;  
 Best Local Similarity 99.7%; Pred. No. 9.9e-140;  
 Matches 299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPTAVCLCLFVVGSGNVVTV 60  
 DB 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPTAVCLCLFVVGSGNVVTV 60

QY 61 MLIGRYDMRTTNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPLLCLRLSLYVGE 120  
 DB 61 MLIGRYDMRTTNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPLLCLRLSLYVGE 120  
 QY 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVNAVALLSAGPFFLVGVE 180  
 DB 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVNAVALLSAGPFFLVGVE 180  
 QY 181 QDPGISVVGGLNGTARIASSPLASPPMLSRAPPPSPGPETAEEAALFSRECRPSA 240  
 DB 181 QDPGISVVGGLNGTARIASSPLASPPMLSRAPPPSPGPETAEEAALFSRECRPSA 240  
 QY 241 QLGALRVMLWTTAYFFLPFLCLSLYGLIGRELWSSRPPLRGPAASGRGRHQTNRVL 300  
 DB 241 QLGALRVMLWTTAYFFLPFLCLSLYGLIGRELWSSRPPLRGPAASGRGRHQTNRVL 300

## RESULT 11

AAB62653  
 ID AAB62653 standard; protein; 386 AA.

AC AAB62653;  
 XX

DT 23-JUL-2001 (first entry)  
 XX

DE Short form of motilin receptor, GPR-38B isoform.  
 XX

KW zsig33; signal transduction; hormone; enzyme; neural development;  
 KW gastric contractility; nutrient uptake; digestive; pancreatic; human;  
 KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;  
 KW glucose; osteopathic; anorectic; vulnery; immunomodulator; GHS-R;  
 KW G-protein coupled receptor; motilin receptor; GPR38; GPR-38B; isoform.  
 XX

OS Homo sapiens.  
 XX

FN WO200138955-A2.  
 XX

PD 31-MAY-2001.  
 XX

PF 22-NOV-2000; 2000WO-US032074.  
 XX

PR 22-NOV-1999; 99US-0166765P.  
 XX

XX (ZYMO ) ZYMOGENETICS INC.  
 XX

XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;  
 XX

XX WPI; 2001-355879/37.  
 XX

DR N-PSDB; AAF83684.  
 XX

XX Forming reversible peptide receptor complex for purifying cell and  
 PT peptides, stimulating signal transduction and modulating hormone  
 PT secretion, involves contacting a receptor with zsig33 polypeptide.  
 XX

XX Disclosure; Page 106-109; 111pp; English.  
 XX

XX The invention relates to a method of forming a reversible peptide-  
 CC receptor complex that involves providing an immobilized receptor, and  
 CC contacting the receptor with a zsig33 peptide (comprising residues 24-37  
 CC of AAB62649), where the receptor binds to the zsig33 peptide. The method  
 CC is useful for purifying cells, purifying a peptide, stimulating signal  
 CC transduction in a cell expressing a receptor. It is also useful for  
 CC modulating secretion of hormones, neural development and/or utilization,  
 CC gastric contractility, nutrient uptake, secretion of digestive and  
 CC pancreatic enzymes and hormones, secretion of insulin-like growth factor  
 CC -I, secretion of non-zsig33 proteins. It is useful for modulating growth  
 CC hormone secretion in a mammal having a disease associated with abnormal  
 CC levels of growth hormone, such as osteoporosis, bone repair, bone  
 CC remodeling, low osteoblast levels, cartilage repair and remodeling,  
 CC skeletal dysplasia, immune suppression, obesity, growth retardation,  
 CC protein catabolic responses after surgery, cachexia, protein loss,  
 CC dwarfism, wound healing and ovulation induction, treating a mammal having

CC a metabolic disorder requiring neurological feedback, such as satiety  
 CC regulation, glucose absorption and metabolism and neuropathy-associated  
 CC gastrointestinal disorders, and stimulating glucose-induced insulin  
 CC release in a mammal. The present sequence represents the short form of  
 CC motilin receptor, GPR-38B (one of the two isoforms of GPR38 which result  
 CC from alternative splicing). GPR38 has homology to the human G-protein  
 CC coupled receptor, GHS-R  
 XX

SQ Sequence 386 AA;

Query Match 73.1%; Score 1575; DB 4; Length 386;  
 Best Local Similarity 99.7%; Pred. No. 9.9e-140;  
 Matches 299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGPEGAREPWPALPCDERRCSPFPALGVPTAVCLCLFVVGVSGNVVTV 60

DB 1 MGSPWNGSDGPEGAREPWPALPCDERRCSPFPALGVPTAVCLCLFVVGVSGNVVTV 60

QY 61 MLIGRYDMRTTNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPLLCLRLSLYVGE 120

DB 61 MLIGRYDMRTTNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPLLCLRLSLYVGE 120

QY 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVNAVALLSAGPFFLVGVE 180

DB 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVNAVALLSAGPFFLVGVE 180

QY 181 QDPGISVVGGLNGTARIASSPLASPPMLSRAPPPSPGPETAEEAALFSRECRPSA 240

DB 181 QDPGISVVGGLNGTARIASSPLASPPMLSRAPPPSPGPETAEEAALFSRECRPSA 240

QY 241 QLGALRVMLWTTAYFFLPFLCLSLYGLIGRELWSSRPPLRGPAASGRGRHQTNRVL 300

DB 241 QLGALRVMLWTTAYFFLPFLCLSLYGLIGRELWSSRPPLRGPAASGRGRHQTNRVL 300

## RESULT 12

AAB68476

ID AAB68476 standard; protein; 271 AA.

AC AAB68476;  
 XX

DT 23-JUL-2001 (first entry)  
 XX

DE Amino acid sequence of a dog motilin receptor exon 1.  
 XX

KW Motilin receptor; gastrointestinal disease; gastric motility disorder;  
 KW gastroparesis; irritable bowel syndrome; diarrhoea.  
 XX

OS Canis sp.  
 XX

PN WO200132710-A1.  
 XX

PD 10-MAY-2001.  
 XX

PF 25-OCT-2000; 2000WO-US029426.  
 XX

PR 29-OCT-1999; 99US-0162264P.  
 XX

XX (MERI ) MERCK & CO INC.  
 XX

XX Tan C, McKee K;  
 XX

XX WPI; 2001-343479/36.  
 XX

DR N-PSDB; AAF85447.  
 XX

XX Novel polypeptides related to dog and rabbit motilin receptor  
 PT polypeptide, comprising unique regions from dog and motilin receptor  
 PT amino acid sequence, useful for identifying compounds for treating  
 PT diarrhea in humans.  
 XX

PS Claim 4; Page 17; 42pp; English.  
 XX

XX The present sequence is encoded by exon 1 of a dog motilin receptor gene.  
 CC



CC The specification describes an unique sequence present in exon 1 of the  
CC motilin receptor, which is not present in human or *Sphaeroides* nephelus  
CC 7537 motilin receptor sequences. The unique nucleic acid sequence is  
CC useful for measuring the ability of a compound to affect motilin receptor  
CC activity. Motilin receptor polynucleotides and polypeptides are used to  
CC identify therapeutic compounds which are useful for treating  
CC gastrointestinal diseases and disorders such as gastric motility  
CC disorders, gastroparesis, irritable bowel syndrome, and diarrhea  
XX  
SQ Sequence 271 AA:

Query Match	53.0%;	Score 1143.5;	DB 4;	Length 271;
Best Local Similarity	76.7%;	Pred. NO. 3e-99;		
Matches 230;	Conservative 13;	Mismatches 28;	Indels 29;	Gaps 4
QY	1	MGSPWNGSDGPEGAREPWPALPCDERRCSPFPFLGALVPVTA	CLCLFVGVSGNVTV	60
DB	1	MGGPGNSDGAEGAQ-----LPCDERLCSPFPFLGALVPVTA	CLGLFVGVSGNLVTV	53
QY	61	MLIGRYDMRTTNLYLGSMAVSDLLILGLHPDLYRLWRSRPWFGL	PLCLRLSLYLVGEG	120
DB	54	LLIGRYDMRTTNLYLGSMAVSDLLILGLHPDLYRLWRSRPWFGL	CLCLRLSLYLVGEG	113
QY	121	CTVATLLHTALSVERYLAICRPLRARVLVITRRVRALIAVLWA	VALLSAGPFLVGVGE	180
DB	114	CTVATLLHTALSVERYLAVCRPLRARALLSRRARALIAALWA	VALLSAAAPFFFLVGVGE	173
QY	181	QDGEISVVGNGTARIASSPLASSPPLWLSRAPPPSPSPGPTAE	AAALFSRECRSPSA	240
DB	174	QDAQ--GPGINGSA RLARA-----PSPPPGPE---AALFSRECR	SPSPS	211
QY	241	OLGALRVLWVTATYAFPLFPLCLLSILYGLIGREIWSRRP	LRGPAAASGRGRHQT	300
DB	212	OLGALRVLWVTATYAFPLFPLCLLCVLGYRIGRELRREGR	PLRGAAASGRGRHQA	271

RESULT 13	
AAV54147	
ID	RAY54147 standard; protein; 363 AA.
XX	
XX	AAV54147;
XX	
DT	12-SEP-2003 (revised)
DT	27-MAR-2000 (first entry)
XX	
DE	The puffer fish motilin receptor protein encoded by clone 75E7.
XX	
XX	Motilin receptor; G-protein coupled receptor; MTL-R1; GPR38;
KW	spliced form; MTL-R1A; MTL-R1B; Gastric motility disorder;
KW	functional defect; neurological disorder; scleroderma; colonoscopy;
KW	paraneoplastic syndrome; radiation induced dysmotility; diabetes;
KW	infection; stress-related motility disorder; psychogenic disorder;
KW	gastroparesis; gastro-oesophageal reflux disease; constipation;
KW	chronic idiopathic pseudo obstruction; acute faecal impaction;
KW	postoperative ileus; gallstones; infantile colic; diarrhoea;
KW	irritable bowel syndrome; non-ulcer dyspepsia; non-cardiac chest pain;
KW	endoscopy; duodenal intubation.

XX	OS	Sphoeroides nephelus.
XX	XX	
XX	PN	WO9964436-A1.
XX	XX	
XX	PD	16-DEC-1999.
XX	XX	
XX	PF	08-JUN-1999; 99WO-US012773.
XX	XX	
XX	PR	12-JUN-1998; 98US-0089098P.
XX	XX	
XX	PA	(MERI ) MERCK & CO INC.
XX	XX	
PI	PI	Feighner SD, Patchett AA, Tan C, McKee K, Macneil D, Howard AD;
PI	PI	Pong S, Smith RG;
XX	XX	

WPI; 2000-105968/09.  
N-PSDB; AAZ45405.

Novel receptor protein for screening compounds used in treating irritable bowel syndrome, constipation and other gastric conditions.

Claim 7; Fig 8; 44pp; English.

The present sequence represents a motilin receptor (clone 75P7) which is related to the human motilin receptor of the invention. The specification describes a G-protein coupled receptor, designated MTU-R1 (also GPR38). Two spliced forms of GPR38 exist, MTU-RIA (see AAY54145) and MTU-R1B (see AAY54146). MTU-RIA is a functional seven transmembrane domain form, and MTU-R1B is a truncated five transmembrane domain form, and the MTU-R1 proteins are used to identify agonists and antagonists which can be used for treating gastric motility disorders, functional defects, disorders secondary to neurological disorders e.g. scleroderma, paraneoplastic syndromes radiation induced dysmotility, diabetes, infections, stress-related motility disorders, psychogenic disorders, gastroparesis, gastro-oesophageal reflux disease, constipation, chronic idiopathic pseudo-obstruction, acute faecal impaction, postoperative ileus, gallstones, infantile colic, irritable bowel syndrome non-ulcer dyspepsia, non-cardiac chest pain and diarrhoea. They can also be used in the preparation for colonoscopy, endoscopy and duodenal intubation. (Updated on 12-SEP-2003 to standardise OS field)

Sequence 363 AA;

Query Match	41.8%;	Score 901;	DB 3;	Length 363;
Best Local Similarity	50.3%;	Pred. No. 3.1e-76;		
Matches 179;	Conservative 56;	Mismatches 77;	Indels 44;	Gaps 5

  

Qy	31	SPPEFGALVFVTA	CLCLFVGVSGNVVTVM	LI	GKRYEDMR	TTT	NLYL	IGSMAVSDLL	IILG	90
Db	31	SLFPASTLIP	VTVCILIFVGV	TGNTMT	ILIIQYFKDM	TKTTT	NLYL	SSMAVSDLV	IFLC	90
Qy	91	LPFDLYDLWRSR	PWVFGLICRL	SLYV	GCGTYATL	HHMTAL	SVERYIAI	CRPR	RLV	150
Db	91	LPFDLYELWKY	VPLFGEAV	CLRVHYI	FE	GCTSA	TIHLTALS	IERVLAIS	FFP	150
Qy	151	TRRRVRALIA	VLMAVALLS	AGPFLF	LVGEVD	PGCISV	VPGLNG	TARIASS	PLASSP	210
Db	151	TRRRVQYII	LALMCFAL	VSAAPTL	FLVGEVD	-----	NET	-----	-----	185
Qy	211	SRAPPPSP	GPSPETAE	AAALFS	RECRSPAQL	--	GALR	VLMLW	TVTATF	268
Db	186	-----	HPD	YNTG	-----	QCKHTG	VAISSGQ	LHIMIW	STTYFF	229
Qy	269	LIGRELWSS	RRPILR	GPAA	SREGRH	QTRK	VLVV	VLAFI	ICWLF	328
Db	230	SIGCKLWKS	NDLQ	GPCAL	ARESHR	QTVK	ILVV	VLAFI	ICWLF	289
Qy	329	MMVFQSV	FNIVAI	QLQFL	YSAL	SINPL	LYNL	ISKY	RAAF	384
Db	290	TAMLSQN	FNWAS	WMVLC	YLSAS	INPVT	YNLSR	KYRAA	KRLFL	344

  

RESULT 14	
AAB68479	
ID AAB68479	standard; protein; 363 AA

RESULT 14
AAB68479
ID AAB6
XX AC
XX AC
DT DT
DT DT
DE DE
XX XX
KW KW
XX XX
OS OS
XX XX

PN WO200132710-A1.  
XX 10-MAY-2001.  
XX 25-OCT-2000; 2000WO-US029426.  
XX 29-OCT-1999; 99US-0162264P.  
XX (MERI ) MERCK & CO INC.  
XX Tan C, McKee K;  
XX WPI; 2001-343479/36.  
XX N-PSDB; AAF85450.  
XX Novel polypeptides related to dog and rabbit motilin receptor  
XX polypeptide, comprising unique regions from dog and motilin receptor  
XX amino acid sequence, useful for identifying compounds for treating  
XX diarrhea in humans.  
XX Disclosure; Page 33-34; 42pp; English.  
XX The present sequence represents a bacterial motilin receptor polypeptide.  
XX The specification describes a unique sequence present in exon 1 of the  
XX dog motilin receptor, which is not present in human or Sphaeroides  
XX nepheus 75E7 motilin receptor sequences. The unique nucleic acid  
XX sequence is useful for measuring the ability of a compound to affect  
XX motilin receptor activity. Motilin receptor polynucleotides and  
XX polypeptides are used to identify therapeutic compounds which are useful  
XX for treating gastrointestinal diseases and disorders such as gastric  
XX motility disorders, gastroparesis, irritable bowel syndrome, and  
XX diarrhoea. (Updated on 06-AUG-2003 to correct OS field.)  
XX Sequence 363 AA;  
SQ  
Query Match 41.8%; Score 901; DB 4; Length 363;  
Best Local Similarity 50.3%; Pred. No. 3.1e-76;  
Matches 179; Conservative 56; Mismatches 77; Indels 44; Gaps 5;  
QY 31 SPFGLGALVPYATVCLCLFVVGVSNNVTVMLIGYRDMRTTNLYLGSMAVSDLLILLG 90  
Db 31 SLFPASTLIPVTVCILIFVVGVTGNTWTIIQYFKDMKTTNLYLSSMAVSDLVIFLC 90  
QY 91 LPFDLYLRWRSPVWFGPCLRLSLYVGEGETATLLHMTALSVERYLAICRPLRVLV 150  
Db 91 LPFDLYLRWLVKVPWLFGEAVCRLYHYIFEGCTSAITLHITALSERYLAISFPLRSKVMV 150  
QY 151 TRRRVRLIALVAVALLSAGPFLVGVQDPGSLVVPGLNGTARIASSPLASSPPLWL 210  
Db 151 TRRRVQYIILALWCALVSAAPTFLVGVGYD-----NET----- 185  
QY 211 SRAPPPSPSPGFTAEAAALFSRECRPSAOL--GALRVMLWVTITAYFELFCLLSILYG 268  
Db 186 ---HPDYNIG-----QCKHTGYAISGQLHIMVSTIYFCFMCMLCLLYG 229  
QY 269 LIGRELSSRRPLRGPAAASGRGHRQKRVLLVVLAFIICWLPFFHVGRIIYINTEDSR 328  
Db 230 SIGCKLWKSNDLQGPCALARSHRQVTKILVVVLAFIICWLPYHIGRNLFQAQVDYD 289  
QY 329 MMYSQYENIVALQIFYLASINPILYNLISKYRAAFAKLLARKSPRGFHRSR 384  
Db 290 TAMLSONFMASVLCYLSASINPVYVNLNGKRYAAAKRLLFHQ-RPKPAHRGQ 344  
RESULT 15  
RAY90666  
ID AAY90666 standard; protein; 366 AA.  
XX  
AC AAY90666;  
XX  
DT 21-AUG-2000 (first entry)  
XX  
DE Human mutant G protein-coupled receptor GHSR (V262K).

XX G protein-coupled receptor; GPCR; constitutively active;  
KW intracellular loop 3; transmembrane domain 6; drug screening; agonist;  
KW antagonist; mutant; mutein.  
XX Homo sapiens.  
OS Synthetic.  
XX WO200022129-A1.  
PN 20-APR-2000.  
PD 12-OCT-1999; 99WO-US023938.  
XX 13-OCT-1998; 98US-00170496.  
PR (AREN-) ARENA PHARM INC.  
PA Behan DP, Chalmers DT, Liaw CW;  
XX WPI; 2000-329165/28.  
XX N-PSDB; AAA30732.  
XX Non-endogenous constitutively activated human G protein-coupled  
XX receptors, useful for identifying agonists for use as pharmaceutical  
XX agents.  
XX Example 2; Page 267-268; 34lpp; English.  
XX The invention relates to constitutively active, non-endogenous versions  
XX of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-  
XX AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743  
XX and AAA30775-A30779). The mutant proteins of the invention contain a  
XX mutation in a portion of the protein comprising intracellular loop 3  
XX (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,  
XX is substituted for an endogenous residue in IC3 at a position 16 amino  
XX acids N-terminal of an endogenous proline in TM6 to form a sequence X-  
XX (AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or  
XX Ala, and is preferably Lys. When the endogenous residue at this position  
XX is Lys, this residue is replaced by His, Arg or preferably Ala. The 15  
XX amino acid stretch between the substituted amino acid and the Pro may be  
XX endogenous, non-endogenous, or a mixture of endogenous and non-endogenous  
XX residues. The constitutively active GPCRs are useful for identifying  
XX antagonists, agonists and partial agonists for use as pharmaceutical  
XX agents. The mutant proteins are also useful in research settings for  
XX elucidating the roles of the receptors in normal and diseased conditions.  
XX Antagonists for a particular GPCR are useful for treating diseases and  
XX disorders associated with that receptor. Because the novel mutant GPCRs  
XX are constitutively active, they can be used directly for screening of  
XX compounds without the need for endogenous ligands. Sequences AAY90643-  
XX AAY90677 and AAY90683-Y90687 the mutant human GPCRs of the invention  
XX Sequence 366 AA;  
SQ  
Query Match 40.1%; Score 864.5; DB 3; Length 366;  
Best Local Similarity 44.7%; Pred. No. 8.7e-73;  
Matches 186; Conservative 59; Mismatches 106; Indels 65; Gaps 9;  
QY 5 WNGSDGEGA-----REPPWPAIAPPD---ERRCSPPLGALVPTAVCLFVVGSGN 56  
Db 2 WNATPSEPFGNLTADLDWDASPGNSDGLQELQFPAPLLAGVTATCTVALFVVGAGN 61  
QY 57 VVTVMILGRYDMRTTNLYLGSMAVSDLLILLGLPDLRLWRSPVWFGPCLRLSLY 116  
Db 62 LITMLVSVSRFRRLKTTNLYLSSNAFSDLLIFLCMPDLRLWQYRPNFNGDLLCKLFQF 121  
QY 117 VGEQCTYATLLHMTALSVERYLAICRPLRVLVTRRRVRLIALVAVALLSAGPFLFL 176  
Db 122 VSESTYATVITLTSVRYFALCFPLRAKVTVTKGRVKLVIFVIWAVAFCSAGPFLVL 181  
QY 177 VGVQDPGIVVPGNLNGTARIASSPLASSPPLMLSRAPPPSPGPTABAAALFSRECR 236  
Db 182 VGVHE-----NCT-----DP--W-----DTNECR 199

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QY 237 PS--PAQLGALRVMLWVTTAYPELPCLSLYGLIGRELWSSRRPLRGPAASGRERGHR 294
Db 200 PTEFAVRSGLLTVMWVSSIFFPVFCUTVLYSLGRKLRRRRGDAVVGASLRDQNHK 259
QY 295 QTKRVLVVVLAFIICWLPFHVGRIIYINTEDS--RMMYFSQYFNIVALQLFYLSASIN 351
Db 260 QTKKMLAVVVVAFILCWLPFHVGRIYLSKSFEPGSLFIQISQYCNLVSVFVLYLSAAN 319
QY 352 PILYNLISKYRAAAFKLLARKSRPRGFHRSRDTAGEVAGDTGGDTVGYTETSAN 407
Db 320 PILYNIMSKKYRVAVFLLIGFEPFSQKSLTLKDESSR-----AWTESSIN 365

```

Search completed: July 4, 2004, 03:07:24  
Job time : 78 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 4, 2004, 03:07:53 ; Search time 23 Seconds  
(without alignments)  
924.778 Million cell updates/sec

Title: US-09-876-252-130

Perfect score: 2156

Sequence: 1 MGSPWNGSDGEGAREPPWP .....DTGSDTVGYTETSANVKTWG 412

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/prodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/prodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/prodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/prodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/prodata/2/iaa/6C\_COMB.pep.\*  
6: /cgn2\_6/prodata/2/iaa/6D\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2149	99.7	412	4	US-09-743-742B-8
2	864.5	40.1	366	4	US-09-170-496D-210
3	859.5	39.9	349	4	US-09-762-661A-2
4	858.5	39.8	366	4	US-09-762-661A-7
5	858.5	39.8	366	4	US-09-743-475-6
6	857.5	39.8	366	3	US-09-743-475-13
7	857.5	39.8	366	4	US-09-077-674-13
8	857.5	39.8	366	4	US-09-170-496D-88
9	857.5	39.8	366	4	US-09-743-742B-7
10	857.5	39.8	366	4	US-09-762-661A-5
11	857.5	39.8	366	4	US-09-364-425B-45
12	857.5	39.8	366	4	US-09-743-475-4
13	857	39.7	353	3	US-09-077-675A-3
14	857.5	39.7	353	4	US-09-077-674-3
15	855.5	39.7	364	3	US-09-077-675A-16
16	855.5	39.7	364	4	US-09-077-674-16
17	855.5	39.7	364	4	US-09-762-661A-6
18	855.5	39.7	364	4	US-09-743-475-3
19	855.5	39.7	364	4	US-09-743-475-5
20	854	39.6	361	3	US-09-077-675A-8
21	854	39.6	361	4	US-09-077-674-8
22	769.5	35.7	302	3	US-09-077-675A-2
23	769.5	35.7	302	4	US-09-077-674-2
24	768.5	35.6	302	3	US-09-077-675A-7
25	768.5	35.6	302	4	US-09-077-674-7
26	668.5	31.0	271	3	US-09-077-675A-12
27	668.5	31.0	271	4	US-09-077-674-12

28	638.5	29.6	289	3	US-09-077-675A-10	Sequence 10, Appl
29	638.5	29.6	289	4	US-09-077-674-10	Sequence 10, Appl
30	627	29.1	289	3	US-09-077-675A-5	Sequence 5, Appl
31	627	29.1	289	4	US-09-077-674-5	Sequence 5, Appl
32	491	22.8	418	4	US-09-743-742B-5	Sequence 5, Appl
33	490.5	22.8	403	4	US-09-170-496D-224	Sequence 224, App
34	484.5	22.5	403	4	US-09-170-496D-114	Sequence 114, App
35	484.5	22.5	403	4	US-09-743-742B-4	Sequence 4, Appl
36	484.5	22.5	403	4	US-09-743-742B-10	Sequence 10, Appl
37	477	22.1	415	4	US-09-545-944-2	Sequence 2, Appl
38	463	21.5	353	1	US-08-118-270-45	Sequence 45, Appl
39	463	21.5	353	5	PCT-US93-08528-45	Sequence 45, Appl
40	456.5	21.2	405	4	US-09-743-742B-2	Sequence 2, Appl
41	456.5	21.2	405	4	US-09-743-742B-11	Sequence 11, Appl
42	407	18.9	410	3	US-08-858-876A-2	Sequence 2, Appl
43	407	18.9	410	3	US-09-472-880-2	Sequence 2, Appl
44	401	18.6	415	4	US-09-743-742B-6	Sequence 6, Appl
45	401	18.6	416	3	US-08-858-876A-4	Sequence 4, Appl

## ALIGNMENTS

## RESULT 1

US-09-743-742B-8  
; Sequence 8, Application US/09743742B  
; Patent No. 6599718  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Qingyun  
; APPLICANT: Howard, Andrew D.  
; APPLICANT: McKee, Karen Kulju  
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RELATED  
; TITLE OF INVENTION: RECEPTORS AND NUCLEIC ACIDS  
; FILE REFERENCE: 20217YP  
; CURRENT APPLICATION NUMBER: US/09/743,742B  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: PCT/US99/15941  
; PRIOR FILING DATE: 1999-07-13  
; PRIOR APPLICATION NUMBER: 60/092,623  
; PRIOR FILING DATE: 1998-07-13  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 412  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-743-742B-8

Query Match 99.7%; Score 2149; DB 4; Length 412;  
Best Local Similarity 99.8%; Pred. No. 2.2e-175;  
Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MGSPWNGSDGEGAREPPWPALPCDDERRCSPFPPLGALVPTAVCLCLFVVGVSQNVVTV	60
DB	1	MGSPWNGSDGEGAREPPWPALPCDDERRCSPFPPLGALVPTAVCLCLFVVGVSQNVVTV	60
QY	61	MLIGRYDMRTTNLYLGSMVSDLLILGLPFDLYRLWRSRPWVFGPLCLSLYVSG	120
DB	61	MLIGRYDMRTTNLYLGSMVSDLLILGLPFDLYRLWRSRPWVFGPLCLSLYVSG	120
QY	121	CTYATLHMTALSVERYLAICRPLARVLVTRRRVRLIAVLWALLSAGPFLVNGVE	180
DB	121	CTYATLHMTALSVERYLAICRPLARVLVTRRRVRLIAVLWALLSAGPFLVNGVE	180
QY	181	QDPGISVVGGLNGTARIASSPLASSPPPLWLSRAPPPSPGPTAAALFSRCRPSA	240
DB	181	QDPGISVVGGLNGTARIASSPLASSPPPLWLSRAPPPSPGPTAAALFSRCRPSA	240
QY	241	QLGALRVMLVTTTAYFFLPFTCLSLYGLICRELWSSRRPLRGPAASGRGRHQTKEVL	300
DB	241	QLGALRVMLVTTTAYFFLPFTCLSLYGLICRELWSSRRPLRGPAASGRGRHQTKEVL	300
QY	301	LVVVLAFTICWLPFHVGRIIYINTEDSRMVFSQVFNIVALQLFVLSASINPLYNLSK	360

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Db 301 LVVLAFLICWLPVHGRIIIVNTSDSRMYFSQYFNIVALQLFYLASINPILYNLSK 360
QY 361 KYRAAAKLLARKSRPRGFRHSRDTAGEVAGDTGGDTGVGTYSANVKTWG 412
Db 361 KYRAAAKLLARKSRPRGFRHSRDTAGEVAGDTGGDTGVGTYSANVKTWG 412

RESULT 2
US-09-170-496D-210
; Sequence 210, Application US/09170496D
; Patent No. 655339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 655339-Endogenous, Constitutively Activated Human G Protein-
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 210
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-210

Query Match 40.1%; Score 864.5; DB 4; Length 366;
Best Local Similarity 44.7%; Pred. No. 6e-66;
Matches 186; Conservative 59; Mismatches 106; Indels 65; Gaps 9;

QY 5 WNGSDGPEGA-----REPPWLPAPCD---ERRCSPPLGALVPVTAVCICLFVVGSGN 56
Db 2 WNAIPEEPGENLTADDDWDASGNDLSGDELLQLPAPLLAGVTATCVAFVVGAGN 61
QY 57 VVTVMILGRIYDMRTTNLYLGSMAYSDLLILGLPDLVRLWRSRPWVFGPILLCRLSLY 116
Db 62 LLETMLVSVRPRELRTTNLYLSSMAFSDLLIFLCMPDLDLVRLWQYRPNWFGDILCKLFQF 121
QY 117 VGECTATILHMTALSVERYLAICRPLRVLVTRRRVRLATVAVLWVALLSAGPPLFL 176
Db 122 VSESCYATVLTITALSVERYFAICFPLRAKVIVTKGRVKLVIFVIWAVAFCSAGPIFVL 181
QY 177 VGVQDPGIGVWPGLNGTARIASSPLASPPMLSRAPPPSGPETAALFSECR 236
Db 182 VGVHE-----NGT-----DP-W-----DTNECR 199
QY 237 PS--PAQLGALRVMLVTTAYFFLPCLSLYLIGLIGRELWSSRRPLRGPAASGRERGRH 294
Db 200 PTEFAVRSGLLTVMWVSSIFFLPVFCITVLYGLIGRLWRGRDGTAGGASLRQNHK 259
QY 295 QTKRVLVVVLAFLICWLPVHGRIIIVNTSDS---RMMYFSQYFNIVALQLFYLASIN 351
Db 260 QTKKMLAVVVFALICWLPVHGRIYFSKSPFSGLEIAISQYCNLVSVFLYLSAAIN 319
QY 352 PILYNLSKKYRAAFAKLLARKSRPRGFRHSRDTAGEVAGDTGGDTGVGTYSAN 407
Db 320 PILYNMSKKYRVAVFELLGFPFSQKLSLTKDESR-----AWTESSIN 365

RESULT 3
US-09-762-661A-2
; Sequence 2, Application US/09762661A
; Patent No. 6645726
; GENERAL INFORMATION:
; APPLICANT: Howard, Andrew D.
; APPLICANT: Palyha, Oksana C.
; APPLICANT: Smith, Roy G.
; APPLICANT: Tan, Carina P.
; TITLE OF INVENTION: CANINE GROWTH HORMONE SECRETAGOGUE
; TITLE OF INVENTION: RECEPTOR
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; FILE REFERENCE: 20207P
; CURRENT APPLICATION NUMBER: US/09/762,661A
; CURRENT FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US99/17915
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: 60/095,960
; PRIOR FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-762-661A-2

Query Match 39.9%; Score 859.5; DB 4; Length 349;
Best Local Similarity 46.2%; Pred. No. 1.5e-65;
Matches 186; Conservative 50; Mismatches 98; Indels 69; Gaps 8;

QY 14 AREPP-----WPALPPCDERRCSPFPLGALVPVTAVCICLFVVGSGNVVTVMLIGRYDM 69
Db 6 AREGPGSAGWDLDF-----LFPAPLLAGVTATCVAFVAGVAGNLLTVLVVRREFL 57
QY 70 RTTNLYLGSMAYSDLLILGLPDLVRLWRSRPWVFGPILLCRLSLYVVGCTYATILHM 129
Db 58 RTTNLYLCSLACSDLLIFLCMPDLDLVRLWQYRPNWFGDILCKLFQFVSGCTYATVLT 117
QY 130 TALSVERYLAICRPLRVLVTRRRVRLATVAVLWVALLSAGPPLFLVGVQDPGIGSWP 189
Db 118 TALSVERYFAICFPLRAKVIVTKGRVKLALLAWAVAFCSAGPIFVLVGVHE----- 170
QY 190 GLNGTARIASSPLASPPMLSRAPPPSGPETAALFSECRPS--PAQLGALRV 247
Db 171 --NGT-----DPRD-----TRECRATEFAVRSGLLTA 195
QY 248 MLWVTTAYFFLPCLSLYLIGLIGRELWSSRRPLRGPAASGRERGRHROTNRVLLVVVLA 307
Db 196 MWVSVVFFLPVFCITVLYGLIGRLWRGRDGTAGGASLRQNHKQVTVLVAVVFAF 255
QY 308 ICWLPFHVGRRIIIVNTSDS---RMMYFSQYFNIVALQLFYLASINPILYNLSKKYRA 364
Db 256 IFCWLPFHVGRYLFKSPFSGLEIAISQYCNLVSVFLYLSAAINPILYNMSKKYRV 315
QY 365 AAFKLLARKSRPRGFRHSRDTAGEVAGDTGGDTGVGTYSAN 407
Db 316 AVFKLLGFPFSQKLSLTKDESR-----AWTESSIN 348

RESULT 4
US-09-762-661A-7
; Sequence 7, Application US/09762661A
; Patent No. 6645726
; GENERAL INFORMATION:
; APPLICANT: Howard, Andrew D.
; APPLICANT: Palyha, Oksana C.
; APPLICANT: Smith, Roy G.
; APPLICANT: Tan, Carina P.
; TITLE OF INVENTION: CANINE GROWTH HORMONE SECRETAGOGUE
; TITLE OF INVENTION: RECEPTOR
; FILE REFERENCE: 20207P
; CURRENT APPLICATION NUMBER: US/09/762,661A
; CURRENT FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US99/17915
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: 60/095,960
; PRIOR FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-762-661A-7
```

Query Match 39.8%; Score 858.5; DB 4; Length 366;  
 Best Local Similarity 44.9%; Pred. No. 1.9e-65;  
 Matches 188; Conservative 55; Mismatches 105; Indels 71; Gaps 10;

QY 5 WNGSDGPEGA-----REPPMPALPCD---ERRCSPPFLGALVPVAVCLCLFVVGVSNG 56  
 DB 2 WNATPSEPGPNLTLPLDGLWDAPPENDSLVEELLPLFPPTLLAGVATCATCVAFVVGIAGN 61

QY 57 VVTVMILGRVDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLMRSRPWFGPILCLSLY 116  
 DB 62 LLTMLVSVRFREMTTNNLYLSSMAFSDLLIFLCMLDLFRLWQYRPNWNLGNLLCKLPQF 121

QY 117 VGECTVATLLHMTALSVERYLAI CRPLRARVLTTRRRVRLIAVLWAVALLSAGPFLFL 176  
 DB 122 VSSECTVATVLTITALSVERYFAICFPPLRAKVVTGKRVKLVILVIVAWAFCSAGPIFVL 181

QY 177 VGVQDPCISVVGFLNGTARIASSPLASPPMLSRAPPSPSGPPTAATAAALFSRECR 236  
 DB 182 VGVGHD-----NGT-----DPRD-----TNECR 199

QY 237 PS--PAQLGALRVMLWVTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASG---RER 291  
 DB 200 ATEFAVRSGLLTVMWVSSVFFLPFLVCLVLSLIGRLW---RRKRGAAVGSRLDQ 256

QY 292 GHRQTRKVLVAVLAFIICWLPFHVGRIIY---INTEDSRMMYFSQYFNIVALQLFYLSA 348  
 DB 257 NHQTVKMLAVVFAFICLPFHVGRIYFSKLEPGSVIEIAQISQYCNLVSVFLFYLSA 316

QY 349 SINPILYNLSKKYRAAFKILLARKSRPRGFRHSRDTAGEVAGDTGDTVGTETSAN 407  
 DB 317 AINPILYNIMSKRYAVAFKILGPEFSQKLSLTKDESSR-----AWTESSIN 365

RESULT 5  
 US-09-743-475-6  
 ; Sequence 6, Application US/09743475  
 ; Patent No. 6682908  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Smith, Roy G.  
 ; APPLICANT: Van der Ploeg, Leonardus H. T.  
 ; APPLICANT: Howard, Andrew D.  
 ; APPLICANT: Zheng, Hui  
 ; APPLICANT: McKee, Karen Kulju  
 ; APPLICANT: Jiang, Michael M.  
 ; TITLE OF INVENTION: MOUSE GROWTH HORMONE SECRETAGOGUE  
 ; FILE REFERENCE: 20218P  
 ; CURRENT APPLICATION NUMBER: US/09/743,475  
 ; CURRENT FILING DATE: 2001-01-10  
 ; PRIOR APPLICATION NUMBER: PCT/US99/15375  
 ; PRIOR FILING DATE: 1999-07-08  
 ; PRIOR APPLICATION NUMBER: 60/092,361  
 ; PRIOR FILING DATE: 1998-07-10  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 6  
 ; LENGTH: 366  
 ; TYPE: PRT  
 ; ORGANISM: Sus scrofa  
 ; US-09-743-475-6

Query Match 39.8%; Score 858.5; DB 4; Length 366;  
 Best Local Similarity 44.9%; Pred. No. 1.9e-65;  
 Matches 188; Conservative 55; Mismatches 105; Indels 71; Gaps 10;

QY 5 WNGSDGPEGA-----REPPMPALPCD---ERRCSPPFLGALVPVAVCLCLFVVGVSNG 56  
 DB 2 WNATPSEPGPNLTLPLDGLWDAPPENDSLVEELLPLFPPTLLAGVATCATCVAFVVGIAGN 61

QY 57 VVTVMILGRVDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLMRSRPWFGPILCLSLY 116  
 DB 62 LLTMLVSVRFREMTTNNLYLSSMAFSDLLIFLCMLDLFRLWQYRPNWNLGNLLCKLPQF 121

QY 117 VGECTVATLLHMTALSVERYLAI CRPLRARVLTTRRRVRLIAVLWAVALLSAGPFLFL 176  
 DB 122 VSSECTVATVLTITALSVERYFAICFPPLRAKVVTGKRVKLVILVIVAWAFCSAGPIFVL 181

QY 177 VGVQDPCISVVGFLNGTARIASSPLASPPMLSRAPPSPSGPPTAATAAALFSRECR 236  
 DB 182 VGVGHD-----NGT-----DPRD-----TNECR 199

QY 237 PS--PAQLGALRVMLWVTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASG---RER 291  
 DB 200 ATEFAVRSGLLTVMWVSSVFFLPFLVCLVLSLIGRLW---RRKRGAAVGSRLDQ 256

QY 292 GHRQTRKVLVAVLAFIICWLPFHVGRIIY---INTEDSRMMYFSQYFNIVALQLFYLSA 348  
 DB 257 NHQTVKMLAVVFAFICLPFHVGRIYFSKLEPGSVIEIAQISQYCNLVSVFLFYLSA 316

QY 349 SINPILYNLSKKYRAAFKILLARKSRPRGFRHSRDTAGEVAGDTGDTVGTETSAN 407  
 DB 317 AINPILYNIMSKRYAVAFKILGPEFSQKLSLTKDESSR-----AWTESSIN 365

RESULT 6  
 US-09-077-675A-13  
 ; Sequence 13, Application US/09077675A  
 ; Patent No. 6242199  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pai, Lee-Yuh  
 ; APPLICANT: Feighner, Scott C.  
 ; APPLICANT: Howard, Andrew D.  
 ; APPLICANT: Pong, Sheng-Shung  
 ; APPLICANT: Van Der Ploeg, Leonardus H.T.  
 ; TITLE OF INVENTION: RECEPTOR ASSAY  
 ; NUMBER OF SEQUENCES: 16  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Merck & Co., Inc.  
 ; STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
 ; CITY: Rahway  
 ; STATE: NJ  
 ; COUNTRY: USA  
 ; ZIP: 07065-0900  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/077,675A  
 ; FILING DATE: 3-JUN-1998  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Cocuzzo, Anna L.  
 ; REGISTRATION NUMBER: 42,452  
 ; REFERENCE/DOCKET NUMBER: 19590P  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 732-594-1273  
 ; TELEFAX: 732-594-4720  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 13:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 366 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-077-675A-13

Query Match 39.8%; Score 857.5; DB 3; Length 366;  
 Best Local Similarity 44.5%; Pred. No. 2.4e-65;  
 Matches 185; Conservative 59; Mismatches 107; Indels 65; Gaps 9;

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QY      5  WNGSDGPEGA-----REPPWALPPCD--BRRCSPPFLGALVPVTAVCLFLVVGVGSEN 56
Db      2  WNAFSEEPGENLTLADLDWASPNDLSGBELLQLFPAPLLAGVATATCVLFFVVGIGN 61

QY     57  VVTVMILGRYDMRTTNNLYLGSMAVSDLLILGLPFDLYRLWRRSRPWPFGFELLCLRLSLY 116
Db     62  LLTMLVVSFRFELRTTNLYLSSNAFSDLLILFLCMLPLDLVRLWQYRPWNFGFDLLCKLQFQ 121

QY    117  VGECSCTATLLHMTALSVERYLATCRPLARVLVTRRVRVALIWLWALLSAGPFFL 176
Db    122  VSECSCTATVLTITALSVERIFALCFPRAKVWVTKGRVKLVIFVIMAVAFCSAGPIFVL 181

QY    177  VGVQDPGISVYPVGINGTARIASSPPLWLSRAPPPSPGPETAEEAALPSRECR 236
Db    182  VGVBEH-----NGT-----DP--W-----DTNECR 199

QY    237  PS--PAQLGALRVMLWVTYATYFFLPFLCLSLYGLIGRLWSSRRPLRGPAASGERGHR 294
Db    200  PTEFAVRSGLLTVMWVSSIEFFLPVFCVLVLYSLIGKLMRRRREGDVAVVGASLDQNHK 259

QY    295  QTKRVLVVLVLAFTICMLPFVFGRIIYINTEDS--RMWYSQYENIVALQLFYLSASIN 351
Db    260  QTVKMLAVVFAFILCMLPFHVGRVLPSPKEPSCLETAQLSQYCNLVSVFLVFLSAAIN 319

QY    352  PILYNLISKYRAAAFKILLARKSRPGRFHSRDTAGVAGDGTGDTVGYTETSAN 407
Db    320  PILYNMISKYRVAVFLLGPEPFSQRKSLTKDSESR-----AWTESSIN 365

```

RESULT 7  
US-09-077-674-13  
Sequence 13, Application US/09077674  
Patent No. 6531314  
GENERAL INFORMATION:  
APPLICANT: Arena, Joseph P.  
APPLICANT: Cully, Doris F.  
APPLICANT: Feighner, Scott D.  
APPLICANT: Howard, Andrew D.  
APPLICANT: Liberator, Paul A.  
APPLICANT: Schaeffer, James M.  
APPLICANT: Van Der ploeg, Leonardus  
TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR FAMILY  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/077,674  
FILING DATE: 3-JUN-1998  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Cocuzzo, Anna L.  
REGISTRATION NUMBER: 42,452  
REFERENCE/DOCKET NUMBER: 19589P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-1273  
TELEFAX: 732-594-4720  
TELEX:  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:

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RESULT 8
US-09-170-496D-88
; Sequence 88, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-88

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[illegible]

QY 117 VGECTYATLLHMTALSVERYLAIKRLARVLTERRVRLIAVLAVALLSAGPFL 176  
Db 122 VSECTYATVLTALSVERYFAICFPLRAKVVTGKVLVFIWAVAFCSAGPIFVL 181  
QY 177 VGVQDPGISVVGANGTARIASSPLASPPILWLSRAPPPSPGPETAEEAALFSRECR 236  
Db 182 VGVHEH-----NGT-----DP--W-----DTNECR 199  
QY 237 PS--PAQIGALRVMLVWTAYFFFLCLSLIYGLIGRELWSSRRPLRGPAAASGRGHR 294  
Db 200 PTEFAVRSGLLTVMVWSSIFFFLPVCLTVLSYIGRKLWRRRGDAVVGASLRDQNHK 259  
QY 295 QTKRVLVVVLAFLICWLPFHVGRYIYINTEDS---RMVFSQYFNIVALQLFYLSASIN 351  
Db 260 QTVKMLAVVFAFILCWLPFHVGRYLFKSPGSLTAQISQYCNLSVFLYLSAAIN 319  
QY 352 PILYNLSKKYRAAFKULLARKSRPGRHRSRDTAGEVAGDTGDTVGYTETSAN 407  
Db 320 PILYNIMSKKYRVAVERLILGFEPFSQKSLTLKDESSR-----AWTESSIN 365

## RESULT 9

US-09-743-742B-7

; Sequence 7, Application US/09743742B

; Patent No. 6599718

; GENERAL INFORMATION:

; APPLICANT: Howard, Andrew D.

; APPLICANT: McKee, Karen Kulju

; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RELATED

; RECEPTORS AND NUCLEIC ACIDS

; FILE REFERENCE: 20217P

; CURRENT APPLICATION NUMBER: US/09/743,742B

; PRIOR FILING DATE: 2001-03-15

; PRIOR APPLICATION NUMBER: PCT/US99/15941

; PRIOR FILING DATE: 1999-07-13

; PRIOR FILING DATE: 1998-07-13

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 366

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-743-742B-7

Query Match 39.8%; Score 857.5; DB 4; Length 366;

Best Local Similarity 44.5%; Pred. No. 2.4e-65;

Matches 185; Conservative 59; Mismatches 107; Indels 65; Gaps 9;

QY 5 WNGSDGPEGA-----REPPWPALPCD---ERRCSPFPLGALVPVTA VCLCLFVVGVSGN 56  
Db 2 WNATPSEEPGNLTADLDWDASFGNDSLGDELILQLFAPILAGVTATCVAFVVGIAGN 61  
QY 57 VVTVMILGRYRDMRTTNLYLGSMAVSDLLILGLPFDLYRLWRSRPVWFGPLCLRLSLY 116  
Db 62 LLTLMVVSRRFELRTTNLYLSSNAFSDLLIFLCMPDLVLWQVYRPNWFGDLCKLQF 121  
QY 117 VGECTYATLLHMTALSVERYLAIKRLARVLTERRVRLIAVLAVALLSAGPFL 176  
Db 122 VSECTYATVLTALSVERYFAICFPLRAKVVTGKVLVFIWAVAFCSAGPIFVL 181  
QY 177 VGVQDPGISVVGANGTARIASSPLASPPILWLSRAPPPSPGPETAEEAALFSRECR 236  
Db 182 VGVHEH-----NGT-----DP--W-----DTNECR 199  
QY 237 PS--PAQIGALRVMLVWTAYFFFLCLSLIYGLIGRELWSSRRPLRGPAAASGRGHR 294  
Db 200 PTEFAVRSGLLTVMVWSSIFFFLPVCLTVLSYIGRKLWRRRGDAVVGASLRDQNHK 259  
QY 295 QTKRVLVVVLAFLICWLPFHVGRYIYINTEDS---RMVFSQYFNIVALQLFYLSASIN 351  
Db 260 QTVKMLAVVFAFILCWLPFHVGRYLFKSPGSLTAQISQYCNLSVFLYLSAAIN 319

## RESULT 11

US-09-364-425B-45

; Sequence 45, Application US/09364425B

; Patent No. 6653086

; GENERAL INFORMATION:

; APPLICANT: Behan, Dominic P.

; APPLICANT: Chalmers, Derek T.

; APPLICANT: Liaw, Chen W.

QY 352 PILYNLSKKYRAAFKULLARKSRPGRHRSRDTAGEVAGDTGDTVGYTETSAN 407  
Db 320 PILYNIMSKKYRVAVERLILGFEPFSQKSLTLKDESSR-----AWTESSIN 365

## RESULT 10

US-09-762-661A-5

; Sequence 5, Application US/09762661A

; Patent No. 6645726

; GENERAL INFORMATION:

; APPLICANT: Howard, Andrew D.

; APPLICANT: Palyha, Oksana C.

; APPLICANT: Smith, Roy G.

; APPLICANT: Tan, Carina P.

; TITLE OF INVENTION: CANINE GROWTH HORMONE SECRETAGOGUE

; RECEPTOR

; FILE REFERENCE: 20207P

; CURRENT APPLICATION NUMBER: US/09/762,661A

; PRIOR FILING DATE: 2001-05-30

; PRIOR APPLICATION NUMBER: PCT/US99/17915

; PRIOR FILING DATE: 1999-08-06

; PRIOR APPLICATION NUMBER: 60/095,960

; PRIOR FILING DATE: 1998-08-10

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 366

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-762-661A-5

Query Match 39.8%; Score 857.5; DB 4; Length 366;

Best Local Similarity 44.5%; Pred. No. 2.4e-65;

Matches 185; Conservative 59; Mismatches 107; Indels 65; Gaps 9;

QY 5 WNGSDGPEGA-----REPPWPALPCD---ERRCSPFPLGALVPVTA VCLCLFVVGVSGN 56  
Db 2 WNATPSEEPGNLTADLDWDASFGNDSLGDELILQLFAPILAGVTATCVAFVVGIAGN 61  
QY 57 VVTVMILGRYRDMRTTNLYLGSMAVSDLLILGLPFDLYRLWRSRPVWFGPLCLRLSLY 116  
Db 62 LLTLMVVSRRFELRTTNLYLSSNAFSDLLIFLCMPDLVLWQVYRPNWFGDLCKLQF 121  
QY 117 VGECTYATLLHMTALSVERYLAIKRLARVLTERRVRLIAVLAVALLSAGPFL 176  
Db 122 VSECTYATVLTALSVERYFAICFPLRAKVVTGKVLVFIWAVAFCSAGPIFVL 181  
QY 177 VGVQDPGISVVGANGTARIASSPLASPPILWLSRAPPPSPGPETAEEAALFSRECR 236  
Db 182 VGVHEH-----NGT-----DP--W-----DTNECR 199  
QY 237 PS--PAQIGALRVMLVWTAYFFFLCLSLIYGLIGRELWSSRRPLRGPAAASGRGHR 294  
Db 200 PTEFAVRSGLLTVMVWSSIFFFLPVCLTVLSYIGRKLWRRRGDAVVGASLRDQNHK 259  
QY 295 QTKRVLVVVLAFLICWLPFHVGRYIYINTEDS---RMVFSQYFNIVALQLFYLSASIN 351  
Db 260 QTVKMLAVVFAFILCWLPFHVGRYLFKSPGSLTAQISQYCNLSVFLYLSAAIN 319  
QY 352 PILYNLSKKYRAAFKULLARKSRPGRHRSRDTAGEVAGDTGDTVGYTETSAN 407  
Db 320 PILYNIMSKKYRVAVERLILGFEPFSQKSLTLKDESSR-----AWTESSIN 365

## RESULT 11

US-09-364-425B-45

; Sequence 45, Application US/09364425B

; Patent No. 6653086

; GENERAL INFORMATION:

; APPLICANT: Behan, Dominic P.

; APPLICANT: Chalmers, Derek T.

; APPLICANT: Liaw, Chen W.



```
; APPLICANT: Lin, I-Lin
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Chen, Ruoping
; TITLE OF INVENTION: Endogenous, Constitutively Activated G Protein-Coupled Orphan Receptor
; FILE REFERENCE: Azen0047
; CURRENT APPLICATION NUMBER: US/09/364,425B
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/094,879
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: 60/106,300
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/110,906
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 45
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-364-425B-45

Query Match      39.8%; Score 857.5; DB 4; Length 366;
Best Local Similarity 44.5%; Pred. No. 2.4e-65;
Matches 185; Conservative 59; Mismatches 107; Indels 65; Gaps 9;

QY      5 WNGSDGPEGA-----REPPWALPPCD---ERRCSPFPLGALVPVTAVCLCLFVVGSGN 56
Db      2 WNAATPSEPGFNLTADLDWDASFGNDSLGLDELQLFPAPLLAGVTATCVAFVVGIA 61

QY      57 VVTVMILGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVGPLLCRLSLY 116
Db      62 LLTMLVSVRPRELRTTNNLYLSSMAFSDLLIFLCMPDLIVRLWQYRPWNFGDLLCKLFQ 121

QY      117 VGECCYATLLHMTALSVRYLAICRPLRARVLVTRRRVRLALIAVLWAVALLSAGPFLFL 176
Db      122 VSECTYATVLTITALSVERYFAICFPLRAKVVTGKRVKLVIFVIAVAFCSAGPFLVL 181

QY      177 VGYEQDGISVWPLNGTARIASSPLASSPPLWSRAPPPSPGPTAATAALFSECR 236
Db      182 VGVHE-----NGT-----DP--W-----DTNECR 199

QY      237 PS--PAQLGALRVMLVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAASGRGRHR 294
Db      200 PTFEAVRSGLLTVMWVSSIFFLPVCLTVLYSLIGRKLWRRRGDAVVGASLRDQNHK 259

QY      295 QTKRVLLVVVLAFLICMLPHVGRRIIYNTEDS---RMVFSQYFNIVALQFLVLSASIN 351
Db      260 QTVKMLAVVVFALICMLPHVGRYLFSSKSFEPGSLIEIAQISQYCNLVSFVLYLSA 319

QY      352 PLYNLISKYRAAFAKLLARKSRPRGHRSDTAGEVAGDTGGDTVGVTETSAN 407
Db      320 PLYNIMSKYRVAVFRLGFEPPFSQKSLTKDESSR-----AWTESSIN 365

RESULT 12
US-09-743-475-4
; Sequence 4, Application US/09743475
; Patent No. 6682908
; GENERAL INFORMATION:
; APPLICANT: Smith, Roy G.
; APPLICANT: Van der Ploeg, Leonardus H. T.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Zheng, Hui
; APPLICANT: McKee, Karen Kulju
; APPLICANT: Jiang, Michael M.
; TITLE OF INVENTION: MOUSE GROWTH HORMONE SECRETAGOGUE
; FILE REFERENCE: 20218P
; CURRENT APPLICATION NUMBER: US/09/743,475
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: PCT/US99/15375
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; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/092,361
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-743-475-4

Query Match      39.8%; Score 857.5; DB 4; Length 366;
Best Local Similarity 44.5%; Pred. No. 2.4e-65;
Matches 185; Conservative 59; Mismatches 107; Indels 65; Gaps 9;

QY      5 WNGSDGPEGA-----REPPWALPPCD---ERRCSPFPLGALVPVTAVCLCLFVVGSGN 56
Db      2 WNAATPSEPGFNLTADLDWDASFGNDSLGLDELQLFPAPLLAGVTATCVAFVVGIA 61

QY      57 VVTVMILGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVGPLLCRLSLY 116
Db      62 LLTMLVSVRPRELRTTNNLYLSSMAFSDLLIFLCMPDLIVRLWQYRPWNFGDLLCKLFQ 121

QY      117 VGECCYATLLHMTALSVRYLAICRPLRARVLVTRRRVRLALIAVLWAVALLSAGPFLFL 176
Db      122 VSECTYATVLTITALSVERYFAICFPLRAKVVTGKRVKLVIFVIAVAFCSAGPFLVL 181

QY      177 VGYEQDGISVWPLNGTARIASSPLASSPPLWSRAPPPSPGPTAATAALFSECR 236
Db      182 VGVHE-----NGT-----DP--W-----DTNECR 199

QY      237 PS--PAQLGALRVMLVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAASGRGRHR 294
Db      200 PTFEAVRSGLLTVMWVSSIFFLPVCLTVLYSLIGRKLWRRRGDAVVGASLRDQNHK 259

QY      295 QTKRVLLVVVLAFLICMLPHVGRRIIYNTEDS---RMVFSQYFNIVALQFLVLSASIN 351
Db      260 QTVKMLAVVVFALICMLPHVGRYLFSSKSFEPGSLIEIAQISQYCNLVSFVLYLSA 319

QY      352 PLYNLISKYRAAFAKLLARKSRPRGHRSDTAGEVAGDTGGDTVGVTETSAN 407
Db      320 PLYNIMSKYRVAVFRLGFEPPFSQKSLTKDESSR-----AWTESSIN 365

RESULT 13
US-09-077-675A-3
; Sequence 3, Application US/09077675A
; Patent No. 6242199
; GENERAL INFORMATION:
; APPLICANT: Pai, Lee-Yuh
; APPLICANT: Feighner, Scott C.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Pong, Sheng-Shung
; APPLICANT: Van Der Ploeg, Leonardus H. T.
; TITLE OF INVENTION: RECEPTOR ASSAY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,675A
; FILING DATE: 3-JUN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19590P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273
; TELEFAX: 732-594-4720
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-077-675A-3

Query Match          39.7%; Score 857; DB 3; Length 353;
Best Local Similarity 46.2%; Pred. No. 2,5e-65;
Matches 185; Conservative 53; Mismatches 96; Indels 66; Gaps 9;

QY 19 WPAIPPCD---ERRCSPPFLGALVPTAVCLCLFVVGSGNVVTVMILGKRYDRMTTNL 75
Db 8 WDAPPENDSLVEELLPLFPPTLLAGVTATCVALFVVGIAGNLLTMLVVSRRFEMRTTNL 67
QY 76 YLGSMVAVSDLLILGLPFDLYLWRSRPNVFPGLCRLSLYVGEGCTYATLLHMTALSVE 135
Db 68 YLSSMAFSDLLIFLCMLDPLFQWYRPNLGNLCKLFFVSESCYATVLTITALSVE 127
QY 136 RYLAICRPLRARVLTTRRRVRLIAVLMAVALLSAGPFLFVGVQDPCGISVVPGLNGTA 195
Db 128 RYFALCFPLRAKVVTKGRVKLVILVIAVAFCSAGPIFVLGVHEH-----NGT- 177
QY 196 RIASSPLASSPPLMLSRAPPPSPGPETAALFSAALFSAALFSAALFSAALFSAALFSA 253
Db 178 -----DPRD-----TNECRATEFAVRSGLLTVMVWVSS 205
QY 254 AVFFLPFLCLSTLYGLIGELWSSRRPLRGPAASG---RERCHROTQKRVLLVVLAFILC 310
Db 206 VFFFLPVFCLTVLYSLIGRKLW---RRKGEAAVSSLRDQNHQKQTVKMLAVVVFALIC 262
QY 311 WLPFHVGRIIY---INTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISKKYRAAAF 367
Db 263 WLPFHVGRIYFSKSLPGSVEIAQISQYCNLVSVFLFVLSAAINPILYNLISKKYRVAVF 322
QY 368 KILLARKSRPRGFRHSRDTAGEVAGDTGGDTVGTYTETSAN 407
Db 323 KLLGPEPFSQKRLSTLKDESSR-----AWTESSIN 352

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## RESULT 14

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US-09-077-674-3
; Sequence 3, Application US/09077674
; Patent No. 6531314
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR FAMILY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 B. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,674
; FILING DATE: 3-JUN-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19589P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-077-674-3

Query Match          39.7%; Score 857; DB 4; Length 353;
Best Local Similarity 46.2%; Pred. No. 2,5e-65;
Matches 185; Conservative 53; Mismatches 96; Indels 66; Gaps 9;

QY 19 WPAIPPCD---ERRCSPPFLGALVPTAVCLCLFVVGSGNVVTVMILGKRYDRMTTNL 75
Db 8 WDAPPENDSLVEELLPLFPPTLLAGVTATCVALFVVGIAGNLLTMLVVSRRFEMRTTNL 67
QY 76 YLGSMVAVSDLLILGLPFDLYLWRSRPNVFPGLCRLSLYVGEGCTYATLLHMTALSVE 135
Db 68 YLSSMAFSDLLIFLCMLDPLFQWYRPNLGNLCKLFFVSESCYATVLTITALSVE 127
QY 136 RYLAICRPLRARVLTTRRRVRLIAVLMAVALLSAGPFLFVGVQDPCGISVVPGLNGTA 195
Db 128 RYFALCFPLRAKVVTKGRVKLVILVIAVAFCSAGPIFVLGVHEH-----NGT- 177
QY 196 RIASSPLASSPPLMLSRAPPPSPGPETAALFSAALFSAALFSAALFSAALFSAALFSA 253
Db 178 -----DPRD-----TNECRATEFAVRSGLLTVMVWVSS 205
QY 254 AVFFLPFLCLSTLYGLIGELWSSRRPLRGPAASG---RERCHROTQKRVLLVVLAFILC 310
Db 206 VFFFLPVFCLTVLYSLIGRKLW---RRKGEAAVSSLRDQNHQKQTVKMLAVVVFALIC 262
QY 311 WLPFHVGRIIY---INTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISKKYRAAAF 367
Db 263 WLPFHVGRIYFSKSLPGSVEIAQISQYCNLVSVFLFVLSAAINPILYNLISKKYRVAVF 322
QY 368 KILLARKSRPRGFRHSRDTAGEVAGDTGGDTVGTYTETSAN 407
Db 323 KLLGPEPFSQKRLSTLKDESSR-----AWTESSIN 352

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## RESULT 15

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US-09-077-675A-16
; Sequence 16, Application US/09077675A
; Patent No. 6242199
; GENERAL INFORMATION:
; APPLICANT: Pai, Lee-Yuh
; APPLICANT: Reighner, Scott C.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Pong, Sheng-Shung
; APPLICANT: Van Der Ploeg, Leonardus H.T.
; TITLE OF INVENTION: RECEPTOR ASSAY

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; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,675A
; FILING DATE: 3-JUN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19590P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 364 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-077-675A-16

Query Match 39.7%; Score 855.5; DB 3; Length 364;
Best Local Similarity 48.0%; Pred. No. 3.5e-65;
Matches 184; Conservative 52; Mismatches 82; Indels 65; Gaps 11;

QY 5 WNGSDGPEGAREP-----PWPALPPCD---ERECSPFPLGALVPVTVAVCLCLFVGVGSG 55
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2 WNAT--PSEEPNPVTLDDWDASPGNDSLDPDLLPLFPAPLLAGTATCATCVAFVVGISG 59
QY 56 NVVTVMILIGRYDMRTTNLYLGSMAVSDLLILGLPDLVLRWSRPWVGPGLCLSL 115
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
60 NLTLVTVSRFRURTNNLYSSMAFSDDLIFLCNPLDLVRLWQYRPNFPGDLLCKLFQ 119
QY 116 YVGGCTYATLLHMTALSVERYLAICRPLRARVLTTRRRVRLIAVLWAVALLSAGPFLF 175
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
120 FVSECTYATVLTITALSVERYFAICFPLRAKVVTGKRVKLVILVIWAVAFCSAGPIFV 179
QY 176 LVGVEQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPEETAALFRREC 235
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
180 LVGVEHE-----NGT-----DPRD-----TNEC 197
QY 236 RPS--PAQLGALVMLVWTYATYFPLFCLILYGLIGRELWSSRRPLRGPAASG---RE 290
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
198 RATEFAVRSGLLTVWVWSSVFFFLPVFCLTVLSLGRKLM--RR--RGDAVAGSLRD 253
QY 291 RGHQTKRVLVVVLAFLICMLPHVGRITVINTEDS---RMMYFSQYFNIVALQLFYLS 347
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
254 QNHKQTVKMLAVVVFATFLCWLPHVGRYLFPSKFSFEGSLBIAQISQYCNLVSFVLFYLS 313
QY 348 ASINPILYNLSKKYRAAFKLL 370
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
314 AAINPILYNLSKKYRAVAFKLL 336
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Search completed: July 4, 2004, 03:11:25  
Job time : 25 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 4, 2004, 03:11:28 ; Search time 78 Seconds  
(without alignments)  
1644.217 Million cell updates/sec

Title: US-09-876-252-130

Perfect score: 2156

Sequence: 1 MGSPWNGSDGEGAREPWP .....DTGGDTVGTTTSANVKTMG 412

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 1276540

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/PTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
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17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2156	100.0	412	12	US-09-876-252-130
2	2156	100.0	412	15	US-10-417-820A-130
3	2156	100.0	412	15	US-10-417-820A-150
4	2156	100.0	412	16	US-10-723-955-130
5	2149	99.7	412	14	US-10-225-567A-473
6	2149	99.7	412	14	US-10-290-078-15
7	2149	99.7	412	14	US-10-318-661-28
8	2149	99.7	412	14	US-10-206-677-2
9	864.5	40.1	366	14	US-10-251-385-210
10	857.5	39.8	366	14	US-10-251-385-88
11	857.5	39.8	366	14	US-10-303-204A-13
12	857.5	39.7	353	14	US-10-303-204A-3
13	855.5	39.7	364	14	US-10-303-204A-16
14	854	39.6	361	14	US-10-303-204A-8
15	769.5	35.7	302	14	US-10-303-204A-2

16	768.5	35.6	302	14	US-10-303-204A-7
17	668.5	31.0	271	14	US-10-303-204A-12
18	638.5	29.6	289	14	US-10-225-567A-140
19	638.5	29.6	289	14	US-10-303-204A-10
20	627	29.1	289	14	US-10-303-204A-5
21	498	23.1	418	11	US-09-826-509-535
22	491	22.8	418	14	US-10-225-567A-207
23	490.5	22.8	403	14	US-10-251-385-224
24	485.5	22.5	445	15	US-10-240-145-53
25	485.5	22.5	445	15	US-10-240-145-139
26	484.5	22.5	403	14	US-10-251-385-114
27	484.5	22.5	403	14	US-10-225-567A-540
28	484.5	22.5	403	14	US-10-290-078-18
29	484.5	22.5	403	15	US-10-353-690-10
30	474	22.0	402	12	US-10-258-423-4
31	474	22.0	412	14	US-10-225-567A-557
32	474	22.0	415	12	US-09-875-076-12
33	474	22.0	415	12	US-09-876-252-12
34	474	22.0	415	12	US-10-258-423-2
35	474	22.0	415	14	US-10-272-883-12
36	474	22.0	415	14	US-10-393-807-12
37	474	22.0	415	15	US-10-417-820A-12
38	474	22.0	415	15	US-10-723-955-12
39	472.5	21.9	395	12	US-10-258-423-6
40	472.5	21.9	396	12	US-10-258-423-8
41	467.5	21.7	426	12	US-10-311-671-1
42	434	20.1	418	15	US-10-369-493-5319
43	430	19.9	419	9	US-09-804-551B-26
44	430	19.9	428	14	US-10-270-333-114
45	414	19.2	410	11	US-09-826-509-537

#### ALIGNMENTS

#### RESULT 1

US-09-876-252-130  
; Sequence 130, Application US/09876252  
; Publication No. US20030018182A1  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Lehmann-Bruinsma, Karin  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Lowitz, Kevin P.  
; APPLICANT: Lin, I-Lin  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Liaw, Chen W.  
; TITLE OF INVENTION: Non-Endogenous Constitutively Activated Human G Protein Coupled Rec  
; FILE REFERENCE: AREN-0054  
; CURRENT APPLICATION NUMBER: US/09/876,252  
; CURRENT FILING DATE: 2001-06-07  
; PRIOR APPLICATION NUMBER: 09/416,760  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: 60/110,060  
; PRIOR FILING DATE: 1998-11-27  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,852  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/123,944  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,945  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,948  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,951  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,946

; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,949  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/152,524  
; PRIOR FILING DATE: 1999-09-03  
; PRIOR APPLICATION NUMBER: 60/151,114  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: 60/108,029  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: 60/136,436  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,439  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,567  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/137,127  
; PRIOR FILING DATE: 1999-05-28  
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; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/141,448  
; PRIOR FILING DATE: 1999-06-29  
; PRIOR APPLICATION NUMBER: 60/136,437  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/156,555  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/156,634  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/156,653  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/157,280  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,294  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,281  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,282  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/156,633  
; PRIOR FILING DATE: 1999-09-29  
; NUMBER OF SEQ ID NOS: 146  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 130  
; LENGTH: 412  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-876-252-130

Query Match 100.0%; Score 2156; DB 12; Length 412;  
Best Local Similarity 100.0%; Pred. NO. 1.7e-168;  
Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MGSPWNGSDGEGAREPPWALPCDERRCSPFLGALVPVTA VCLCLFVVGVSGNVVTV 60  
Db 1 MGSPWNGSDGEGAREPPWALPCDERRCSPFLGALVPVTA VCLCLFVVGVSGNVVTV 60  
Qy 61 MLIGRYDMRTTNLYLGSMAVSDLLILGLPFDLYLRWRSPWVFGFLCRLSLYVGE 120  
Db 61 MLIGRYDMRTTNLYLGSMAVSDLLILGLPFDLYLRWRSPWVFGFLCRLSLYVGE 120  
Qy 121 CTYATLLHMTALSVERYIAICRPIRARVLTTRRRVRLIAVLAVALLSAGPFLVGV 180  
Db 121 CTYATLLHMTALSVERYIAICRPIRARVLTTRRRVRLIAVLAVALLSAGPFLVGV 180  
Qy 181 QDPGISVVGNGTARIASSPLASSPPLWLSRAPPSPSPETAEEAALFSRECRSPA 240  
Db 181 QDPGISVVGNGTARIASSPLASSPPLWLSRAPPSPSPETAEEAALFSRECRSPA 240  
Qy 241 QLGALRVMLVWTYATFFLPFLCRLSLYGLIGRELWSSRRPLRGPAASGRERGHRTKRV 300  
Db 241 QLGALRVMLVWTYATFFLPFLCRLSLYGLIGRELWSSRRPLRGPAASGRERGHRTKRV 300  
Qy 301 LVVVLAFIICWLPHVGRITIIYNTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360  
Db 301 LVVVLAFIICWLPHVGRITIIYNTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360

Db 301 LVVVLAFIICWLPHVGRITIIYNTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360  
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Db 361 KYRAAFAFKLLARKSRPRGFHRSRDITAGEVAGDTGGDTVGTYTETSANVKTMG 412  
RESULT 2  
US-10-417-820A-130  
; Sequence 130, Application US/10417820A  
; Publication No. US20030229216A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lowitz, Kevin  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Behan, Dominic P.  
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: 7.US28.CON  
; CURRENT APPLICATION NUMBER: US/10/417,820A  
; CURRENT FILING DATE: 2003-04-16  
; PRIOR APPLICATION NUMBER: 09/416,760  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 09/170,496  
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; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/123,944  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,945  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,948  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,951  
; PRIOR FILING DATE: 1999-03-12  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 155  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 130  
; LENGTH: 412  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-417-820A-130

Query Match 100.0%; Score 2156; DB 15; Length 412;  
Best Local Similarity 100.0%; Pred. NO. 1.7e-168;  
Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MGSPWNGSDGEGAREPPWALPCDERRCSPFLGALVPVTA VCLCLFVVGVSGNVVTV 60  
Db 1 MGSPWNGSDGEGAREPPWALPCDERRCSPFLGALVPVTA VCLCLFVVGVSGNVVTV 60  
Qy 61 MLIGRYDMRTTNLYLGSMAVSDLLILGLPFDLYLRWRSPWVFGFLCRLSLYVGE 120  
Db 61 MLIGRYDMRTTNLYLGSMAVSDLLILGLPFDLYLRWRSPWVFGFLCRLSLYVGE 120  
Qy 121 CTYATLLHMTALSVERYIAICRPIRARVLTTRRRVRLIAVLAVALLSAGPFLVGV 180  
Db 121 CTYATLLHMTALSVERYIAICRPIRARVLTTRRRVRLIAVLAVALLSAGPFLVGV 180  
Qy 181 QDPGISVVGNGTARIASSPLASSPPLWLSRAPPSPSPETAEEAALFSRECRSPA 240  
Db 181 QDPGISVVGNGTARIASSPLASSPPLWLSRAPPSPSPETAEEAALFSRECRSPA 240  
Qy 241 QLGALRVMLVWTYATFFLPFLCRLSLYGLIGRELWSSRRPLRGPAASGRERGHRTKRV 300  
Db 241 QLGALRVMLVWTYATFFLPFLCRLSLYGLIGRELWSSRRPLRGPAASGRERGHRTKRV 300

Db 241 QLGALRVMLWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRERGHRTKRVL 300  
QY 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQOLFYLASINPILYNLSK 360  
Db 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQOLFYLASINPILYNLSK 360  
QY 361 KYRAAFKLLARKSRPRGFHRSRDTAGEVAGDTGGDTGVGTETTSANVKTWG 412  
Db 361 KYRAAFKLLARKSRPRGFHRSRDTAGEVAGDTGGDTGVGTETTSANVKTWG 412

RESULT 3  
US-10-417-820A-150  
; Sequence 150, Application US/10417820A  
; Publication No. US20030229216A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lowitz, Kevin  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Behan, Dominic P.  
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: 7.US28.CON  
; CURRENT APPLICATION NUMBER: US/10/417,820A  
; PRIOR FILING DATE: 2003-04-16  
; PRIOR APPLICATION NUMBER: 09/416,760  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: 60/110,060  
; PRIOR FILING DATE: 1998-11-27  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1998-02-16  
; PRIOR APPLICATION NUMBER: 60/121,852  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/123,944  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,945  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,948  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,951  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 155  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 150  
; LENGTH: 412  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-417-820A-150

Query Match 100.0%; Score 2156; DB 15; Length 412;  
Best Local Similarity 100.0%; Pred. No. 1.7e-168;  
Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTAVALCLFVVGVSNNVTV 60  
Db 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTAVALCLFVVGVSNNVTV 60

QY 61 MLIGRYDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPLCLSLYVGE 120  
Db 61 MLIGRYDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPLCLSLYVGE 120

QY 121 CTYATLLHMTALSVERYLAI CRFLARVLVTRRRVALLI AVLWALLSAGPFLVLVGE 180  
Db 121 CTYATLLHMTALSVERYLAI CRFLARVLVTRRRVALLI AVLWALLSAGPFLVLVGE 180

QY 181 QDPGIVVPGINGTARIASSPPLWLSRAPPPSPGPTAAALFSRECRPSA 240

Db 181 QDPGIVVPGINGTARIASSPPLWLSRAPPPSPGPTAAALFSRECRPSA 240  
QY 241 QLGALRVMLWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRERGHRTKRVL 300  
Db 241 QLGALRVMLWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRERGHRTKRVL 300  
QY 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQOLFYLASINPILYNLSK 360  
Db 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQOLFYLASINPILYNLSK 360  
QY 361 KYRAAFKLLARKSRPRGFHRSRDTAGEVAGDTGGDTGVGTETTSANVKTWG 412  
Db 361 KYRAAFKLLARKSRPRGFHRSRDTAGEVAGDTGGDTGVGTETTSANVKTWG 412

RESULT 4  
US-10-723-955-130  
; Sequence 130, Application US/10723955  
; Publication No. US20040110238A1  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Lin, I-Lin  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lehman-Bruinsma, Karin  
; APPLICANT: Lowitz, Kevin P.  
; APPLICANT: Dang, Huang T.  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Gore, Martin  
; APPLICANT: White, Carol  
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: 7.US29.CON  
; CURRENT APPLICATION NUMBER: US/10/723,955  
; PRIOR FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: 10/417,820  
; PRIOR FILING DATE: 2003-4-16  
; PRIOR APPLICATION NUMBER: 09/416,760  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: 60/110,060  
; PRIOR FILING DATE: 1998-11-27  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,852  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/123,944  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,945  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,948  
; PRIOR FILING DATE: 1999-03-12  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 148  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 130  
; LENGTH: 412  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-723-955-130

Query Match 100.0%; Score 2156; DB 16; Length 412;  
Best Local Similarity 100.0%; Pred. No. 1.7e-168;  
Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTAVALCLFVVGVSNNVTV 60  
Db 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTAVALCLFVVGVSNNVTV 60

QY 61 MLIGRYDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPLCLSLYVGE 120

Db 61 MLIGRYDMRTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRWFWGPLLCLRLSLVVGEG 120  
QY 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPEFLVGVGE 180  
Db 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPEFLVGVGE 180  
QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPGTAAALFSSRECRPSA 240  
Db 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPGTAAALFSSRECRPSA 240  
QY 241 QLGALRVMLWVTYAYFFLPCLSLIYGLIGRELWSSRRPLRGAASGRGRHQRKVL 300  
Db 241 QLGALRVMLWVTYAYFFLPCLSLIYGLIGRELWSSRRPLRGAASGRGRHQRKVL 300  
QY 301 LVVLAIFIICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360  
Db 301 LVVLAIFIICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360  
QY 361 KYRAAFAKLLARKSRPRGFHRSRDTAGEVAGDTGDTGVGTSETSANVKTMG 412  
Db 361 KYRAAFAKLLARKSRPRGFHRSRDTAGEVAGDTGDTGVGTSETSANVKTMG 412  
RESULT 5  
US-10-225-567A-473  
; Sequence 473, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: LifeSpan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burner, Glenna C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 473  
; LENGTH: 412  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-225-567A-473  
Query Match 99.7%; Score 2149; DB 14; Length 412;  
Best Local Similarity 99.8%; Pred. No. 6.3e-168;  
Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MGSPWNGSDGPEGAREPPWLPALPCDERRCSPPLGALVPVTAVCLFLVGVSGNVTV 60  
Db 1 MGSPWNGSDGPEGAREPPWLPALPCDERRCSPPLGALVPVTAVCLFLVGVSGNVTV 60  
QY 61 MLIGRYDMRTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRWFWGPLLCLRLSLVVGEG 120  
Db 61 MLIGRYDMRTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRWFWGPLLCLRLSLVVGEG 120  
QY 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPEFLVGVGE 180  
Db 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPEFLVGVGE 180  
QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPGTAAALFSSRECRPSA 240  
Db 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPGTAAALFSSRECRPSA 240  
QY 241 QLGALRVMLWVTYAYFFLPCLSLIYGLIGRELWSSRRPLRGAASGRGRHQRKVL 300  
Db 241 QLGALRVMLWVTYAYFFLPCLSLIYGLIGRELWSSRRPLRGAASGRGRHQRKVL 300  
QY 301 LVVLAIFIICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360  
Db 301 LVVLAIFIICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360

Db 301 LVVLAIFIICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360  
QY 361 KYRAAFAKLLARKSRPRGFHRSRDTAGEVAGDTGDTGVGTSETSANVKTMG 412  
Db 361 KYRAAFAKLLARKSRPRGFHRSRDTAGEVAGDTGDTGVGTSETSANVKTMG 412  
RESULT 6  
US-10-290-078-15  
; Sequence 15, Application US/102900078  
; Publication No. US20030124596A1  
; GENERAL INFORMATION:  
; APPLICANT: Carroll, Joseph A.  
; TITLE OF INVENTION: Methods and Compositions for Treating  
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,  
; FILE REFERENCE: 14395, 14618, 17692 or 58874  
; FILE REFERENCE: MPI2001-288P1(W)  
; CURRENT APPLICATION NUMBER: US/10/290,078  
; CURRENT FILING DATE: 2002-11-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 412  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-290-078-15  
Query Match 99.7%; Score 2149; DB 14; Length 412;  
Best Local Similarity 99.8%; Pred. No. 6.3e-168;  
Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MGSPWNGSDGPEGAREPPWLPALPCDERRCSPPLGALVPVTAVCLFLVGVSGNVTV 60  
Db 1 MGSPWNGSDGPEGAREPPWLPALPCDERRCSPPLGALVPVTAVCLFLVGVSGNVTV 60  
QY 61 MLIGRYDMRTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRWFWGPLLCLRLSLVVGEG 120  
Db 61 MLIGRYDMRTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRWFWGPLLCLRLSLVVGEG 120  
QY 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPEFLVGVGE 180  
Db 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPEFLVGVGE 180  
QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPGTAAALFSSRECRPSA 240  
Db 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPGTAAALFSSRECRPSA 240  
QY 241 QLGALRVMLWVTYAYFFLPCLSLIYGLIGRELWSSRRPLRGAASGRGRHQRKVL 300  
Db 241 QLGALRVMLWVTYAYFFLPCLSLIYGLIGRELWSSRRPLRGAASGRGRHQRKVL 300  
QY 301 LVVLAIFIICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360  
Db 301 LVVLAIFIICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360  
QY 361 KYRAAFAKLLARKSRPRGFHRSRDTAGEVAGDTGDTGVGTSETSANVKTMG 412  
Db 361 KYRAAFAKLLARKSRPRGFHRSRDTAGEVAGDTGDTGVGTSETSANVKTMG 412  
RESULT 7  
US-10-318-661-28  
; Sequence 28, Application US/10318661  
; Publication No. US20030167476A1  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Bruce R.  
; TITLE OF INVENTION: Selective Target Cell Activation By  
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated  
; FILE REFERENCE: UCAL-049C1P2  
; CURRENT APPLICATION NUMBER: US/10/318,661  
; CURRENT FILING DATE: 2003-05-05  
; PRIOR APPLICATION NUMBER: US 09/341,446

;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: PCT/US97/05334  
;; PRIOR FILING DATE: 1997-03-25  
;; PRIOR APPLICATION NUMBER: US 08/622,348  
;; PRIOR FILING DATE: 1996-03-26  
;; NUMBER OF SEQ ID NOS: 28  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 28  
;; LENGTH: 412  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-318-661-28

Query Match 99.7%; Score 2149; DB 14; Length 412;  
Best Local Similarity 99.8%; Pred. No. 6.3e-166;  
Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGPEGAREPPWPALPPCDERRCSPFFPLGALVPVTAVALCLCLFVVGSGNVVTV 60  
DB 1 MGSPWNGSDGPEGAREPPWPALPPCDERRCSPFFPLGALVPVTAVALCLCLFVVGSGNVVTV 60  
QY 61 MLIORYDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPFLCRLSLYVGE 120  
DB 61 MLIORYDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPFLCRLSLYVGE 120  
QY 121 CTYATLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGV 180  
DB 121 CTYATLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGV 180  
QY 181 QDPGISVVGGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240  
DB 181 QDPGISVVGGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240  
QY 241 QLGALRVMLWTTAYFFLPFLCCLSYLIGLIGRELWSSRRPLRGPAASGRERGHROTQV 300  
DB 241 QLGALRVMLWTTAYFFLPFLCCLSYLIGLIGRELWSSRRPLRGPAASGRERGHROTQV 300  
QY 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQVFNIVALQFLYLSASINPILYNLISK 360  
DB 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQVFNIVALQFLYLSASINPILYNLISK 360  
QY 361 KYRAAAFKLLARKSRPRGHRSDTAGVAGDTGGDTGVGTSTANVKTWG 412  
DB 361 KYRAAAFKLLARKSRPRGHRSDTAGVAGDTGGDTGVGTSTANVKTWG 412

## RESULT 8

US-10-206-677-2  
;; Sequence 2, Application US/10206677  
;; Publication No. US20030186336A1  
;; GENERAL INFORMATION:  
;; APPLICANT: LifeSpan Biosciences, Inc.  
;; APPLICANT: Brown, Joseph P.  
;; APPLICANT: Burner, Glenna C.  
;; APPLICANT: Roush, Christine L.  
;; APPLICANT: Kulaender, Bruce G.  
;; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS RELATED TO  
;; FILE REFERENCE: 1920-1-8  
;; CURRENT APPLICATION NUMBER: US/10/206,677  
;; CURRENT FILING DATE: 2002-11-06  
;; PRIOR APPLICATION NUMBER: 60/250,251  
;; PRIOR FILING DATE: 2000-11-29  
;; PRIOR APPLICATION NUMBER: 60/250,452  
;; PRIOR FILING DATE: 2000-11-30  
;; NUMBER OF SEQ ID NOS: 6  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 2  
;; LENGTH: 412  
;; TYPE: PRT  
;; ORGANISM: Homo Sapiens  
US-10-206-677-2

Query Match 99.7%; Score 2149; DB 14; Length 412;  
Best Local Similarity 99.8%; Pred. No. 6.3e-166;  
Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGPEGAREPPWPALPPCDERRCSPFFPLGALVPVTAVALCLCLFVVGSGNVVTV 60  
DB 1 MGSPWNGSDGPEGAREPPWPALPPCDERRCSPFFPLGALVPVTAVALCLCLFVVGSGNVVTV 60  
QY 61 MLIORYDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPFLCRLSLYVGE 120  
DB 61 MLIORYDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPFLCRLSLYVGE 120  
QY 121 CTYATLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGV 180  
DB 121 CTYATLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGV 180  
QY 181 QDPGISVVGGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240  
DB 181 QDPGISVVGGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240  
QY 241 QLGALRVMLWTTAYFFLPFLCCLSYLIGLIGRELWSSRRPLRGPAASGRERGHROTQV 300  
DB 241 QLGALRVMLWTTAYFFLPFLCCLSYLIGLIGRELWSSRRPLRGPAASGRERGHROTQV 300  
QY 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQVFNIVALQFLYLSASINPILYNLISK 360  
DB 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQVFNIVALQFLYLSASINPILYNLISK 360  
QY 361 KYRAAAFKLLARKSRPRGHRSDTAGVAGDTGGDTGVGTSTANVKTWG 412  
DB 361 KYRAAAFKLLARKSRPRGHRSDTAGVAGDTGGDTGVGTSTANVKTWG 412

## RESULT 9

US-10-251-385-210  
;; Sequence 210, Application US/10251385  
;; Publication No. US20030105292A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Behan, Dominic P.  
;; APPLICANT: Chalmers, Derek T.  
;; APPLICANT: Liaw, Chen W.  
;; TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G  
;; TITLE OF INVENTION: Protein-Coupled  
;; TITLE OF INVENTION: Receptors  
;; FILE REFERENCE: AREN-0040  
;; CURRENT APPLICATION NUMBER: US/10/251,385  
;; CURRENT FILING DATE: 2002-09-20  
;; PRIOR APPLICATION NUMBER: US/09/170,496  
;; PRIOR FILING DATE: 1998-10-13  
;; NUMBER OF SEQ ID NOS: 294  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 210  
;; LENGTH: 366  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-251-385-210

Query Match 40.1%; Score 864.5; DB 14; Length 366;  
Best Local Similarity 44.7%; Pred. No. 1.3e-62;  
Matches 186; Conservative 59; Mismatches 106; Indels 65; Gaps 9;

QY 5 WNGSDGPEGA-----RBPWPALPPCD---ERRCSPFLGALVPVTAVALCLCLFVVGSGN 56  
DB 2 WNATPSEEPGNLTADLDWDASFGNDSLGDELLQFPAPLAGVATCTVALFVVGIAKN 61  
QY 57 VVTWNLIGRYDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPFLCRLSLY 116  
DB 62 LLTMLVWSRFRRLRTTNNLYLSSMAFSDLLIFLCMLDVLRLWQVYRPNWFGDLCKLQF 121  
QY 117 VGECTATLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFL 176  
DB 122 VSECTATLITALSVERYFAICFLRAKVVVTKGRKLVIFVIAVAFCSAGPIFVL 181



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QY 177 VGVEQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAABAAALFSRECR 236
Db 182 VGVHE-----NGT-----DP--W-----DINECR 199
QY 237 PS--PAQGLALRMLVMTTAYFFLPCLSLYGLIGREIMSSRRPLRGPAAASGRGRGHR 294
Db 200 PTEFAVRSGLLTVMWVSSIFFLPVCLTVLSLIGRKLWRRRRGDVAVGASLRDQNHK 259
QY 295 QTKRVLVVLAFIICWLPFHVGRIIYINTEDS---RMVFSQYFNIVALQLPYLSASIN 351
Db 260 QTKMGLAVVVFAPILCWLPFHVGRYLFKSFEPGSLIEIAISQYCNLVSVFLYLSAAN 319
QY 352 PILYNLSKKYRAAFAKLLARKSRPRGHRSDTAGVAGDTGGTVGYTTTSAN 407
Db 320 PILYNMSKKYRVAVFRLIGFEPFSQKSLTKDESSR-----AWTESSIN 365

RESULT 10
US-10-251-385-88
; Sequence 88, Application US/10251385
; Publication No. US20030105292A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G
; TITLE OF INVENTION: Protein-Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/10/251,385
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 88
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-251-385-88

Query Match 39.8%; Score 857.5; DB 14; Length 366;
Best Local Similarity 44.5%; Pred. No. 4.8e-62;
Matches 185; Conservative 59; Mismatches 107; Indels 65; Gaps 9;

QY 5 WNGSDGPEGA-----REPPWALPPCD---ERRCSPPFLGALVPVTAVCLCLFVVGSGN 56
Db 2 WNATPSEEPGNLTADLDWDASPGNDSLGLDELQLFPAPLLAGVTATCVALFVVGIAGN 61
QY 57 VVTVMILIGRYDMRTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPLLCRSLY 116
Db 62 LNTMLVVSFRRLRTTNNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLFQF 121
QY 117 VEGGCTATLLHMTALSVERYLAICRPLRVLVTRRRVRLTAVLWAVALLSAGPFLFL 176
Db 122 VSSCTATVLTITALSVERYFAICPLRAKVVTGKRVKLVIFVIAWAFCSAGPITFVL 181
QY 177 VGVEQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAABAAALFSRECR 236
Db 182 VGVHE-----NGT-----DP--W-----DINECR 199
QY 237 PS--PAQGLALRMLVMTTAYFFLPCLSLYGLIGREIMSSRRPLRGPAAASGRGRGHR 294
Db 200 PTEFAVRSGLLTVMWVSSIFFLPVCLTVLSLIGRKLWRRRRGDVAVGASLRDQNHK 259
QY 295 QTKRVLVVLAFIICWLPFHVGRIIYINTEDS---RMVFSQYFNIVALQLPYLSASIN 351
Db 260 QTKMGLAVVVFAPILCWLPFHVGRYLFKSFEPGSLIEIAISQYCNLVSVFLYLSAAN 319
QY 352 PILYNLSKKYRAAFAKLLARKSRPRGHRSDTAGVAGDTGGTVGYTTTSAN 407
Db 320 PILYNMSKKYRVAVFRLIGFEPFSQKSLTKDESSR-----AWTESSIN 365

RESULT 12
US-10-303-204A-13
; Sequence 3, Application US/10303204A
; Publication No. US20030106614A1
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
```

```
RESULT 11
US-10-303-204A-13
; Sequence 13, Application US/10303204A
; Publication No. US20030106614A1
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris E.
; APPLICANT: Feigener, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus H. T.
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR
; TITLE OF INVENTION: FAMILY
; FILE REFERENCE: 19589PCA
; CURRENT APPLICATION NUMBER: US/10/303,204A
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 09/077,674
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US96/19445
; PRIOR FILING DATE: 1996-12-10
; PRIOR APPLICATION NUMBER: 60/018,962
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 60/008,582
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 366
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-303-204A-13

Query Match 39.8%; Score 857.5; DB 14; Length 366;
Best Local Similarity 44.5%; Pred. No. 4.8e-62;
Matches 185; Conservative 59; Mismatches 107; Indels 65; Gaps 9;

QY 5 WNGSDGPEGA-----REPPWALPPCD---ERRCSPPFLGALVPVTAVCLCLFVVGSGN 56
Db 2 WNATPSEEPGNLTADLDWDASPGNDSLGLDELQLFPAPLLAGVTATCVALFVVGIAGN 61
QY 57 VVTVMILIGRYDMRTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPLLCRSLY 116
Db 62 LNTMLVVSFRRLRTTNNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLFQF 121
QY 117 VEGGCTATLLHMTALSVERYLAICRPLRVLVTRRRVRLTAVLWAVALLSAGPFLFL 176
Db 122 VSSCTATVLTITALSVERYFAICPLRAKVVTGKRVKLVIFVIAWAFCSAGPITFVL 181
QY 177 VGVEQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAABAAALFSRECR 236
Db 182 VGVHE-----NGT-----DP--W-----DINECR 199
QY 237 PS--PAQGLALRMLVMTTAYFFLPCLSLYGLIGREIMSSRRPLRGPAAASGRGRGHR 294
Db 200 PTEFAVRSGLLTVMWVSSIFFLPVCLTVLSLIGRKLWRRRRGDVAVGASLRDQNHK 259
QY 295 QTKRVLVVLAFIICWLPFHVGRIIYINTEDS---RMVFSQYFNIVALQLPYLSASIN 351
Db 260 QTKMGLAVVVFAPILCWLPFHVGRYLFKSFEPGSLIEIAISQYCNLVSVFLYLSAAN 319
QY 352 PILYNLSKKYRAAFAKLLARKSRPRGHRSDTAGVAGDTGGTVGYTTTSAN 407
Db 320 PILYNMSKKYRVAVFRLIGFEPFSQKSLTKDESSR-----AWTESSIN 365

RESULT 12
US-10-303-204A-13
; Sequence 3, Application US/10303204A
; Publication No. US20030106614A1
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
```



; PRIOR FILING DATE: 1996-12-10  
; PRIOR APPLICATION NUMBER: 60/018,962  
; PRIOR FILING DATE: 1996-06-06  
; PRIOR APPLICATION NUMBER: 60/008,582  
; PRIOR FILING DATE: 1995-12-13  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 361  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-303-204A-8

Query Match 39.6%; Score 854; DB 14; Length 361;  
Best Local Similarity 45.8%; Pred. No. 9,1e-62;  
Matches 182; Conservative 57; Mismatches 98; Indels 60; Gaps 8;

QY 19 WPAIPCCD---ERRCSPFPLGALVPVTAVCLCLFVVGSGNVVTVMLIGRYDMRTTNL 75  
Db 16 WDASPGNDSIGDELLQLFPAPLLAGVTATCVAFVVGIAGNLLTMLVWSRFRELRTTNL 75  
QY 76 YLGSMAVSDLLILGLPFDLYLWRSRPVVGPELLCLSLYVCEGCTYATLLHMTALSVE 135  
Db 76 YLSSMAFSDLLIFLCMLDLRLWQTRPNFGDLCKLFQFVSECTYATVITITALSVE 135  
QY 136 RYLAICRPLRARVLTTRRRVRLIAVLWAVALLSAGPFLFVGVQDPGISVVPGLNGTA 195  
Db 136 RYFAICFPLRAKVVTGKRVKLVIFVIMAVAFCSAGPIFVLGVGHE-----NGT- 185  
QY 196 RIASSPLASSPPLWLSRAPPPSPGPETAARAAALFSRECRPS--PAQIGALRVMLWVTT 253  
Db 186 -----DP--W-----DTNECRTEFAVRSGLLTVMVVWS 213  
QY 254 AYFFLPFCLSLIYGLIGRELWSSRRPLRGPAASGRGHRGROTQKRVLLVWLAFICWLP 313  
Db 214 IFFFLPVFCLTVLYSLIGKLRERRGDAVGNLSDQNHKQTVKMLAVVFAFICWLP 273  
QY 314 FHVGRITTYINTEDS-----RMVYSQYENIVALQLFYLSASINPILYNLSKRYRAAFKLL 370  
Db 274 FHVGRYLFKSPFPGSLIAQISQYCNLVSFVLFYLSAAINPILYNLSKRYRAVAVRLL 333  
QY 371 LARKSRPRGFRHSRDTAGEVAGDTGGDTGYTETSAN 407  
Db 334 GPFPFSQKRLSTLKDESSR-----AWTESSIN 360

## RESULT 15

US-10-303-204A-2  
; Sequence 2, Application US/10303204A  
; Publication No. US20030166144A1  
; GENERAL INFORMATION:  
; APPLICANT: Arena, Joseph P.  
; APPLICANT: Cully, Doris F.  
; APPLICANT: Feighner, Scott D.  
; APPLICANT: Howard, Andrew D.  
; APPLICANT: Liberator, Paul A.  
; APPLICANT: Schaeffer, James M.  
; APPLICANT: Van Der Ploeg, Leonardus H. T.  
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR  
; TITLE OF INVENTION: FAMILY  
; FILE REFERENCE: 19589PCA  
; CURRENT APPLICATION NUMBER: US/10/303,204A  
; CURRENT FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 09/077,674  
; PRIOR FILING DATE: 1998-06-03  
; PRIOR APPLICATION NUMBER: PCT/US96/19445  
; PRIOR FILING DATE: 1996-12-10  
; PRIOR APPLICATION NUMBER: 60/018,962  
; PRIOR FILING DATE: 1996-06-06  
; PRIOR APPLICATION NUMBER: 60/008,582  
; PRIOR FILING DATE: 1995-12-13  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2  
; LENGTH: 302  
; TYPE: PRT  
; ORGANISM: sus scrofa  
US-10-303-204A-2

Query Match 35.7%; Score 769.5; DB 14; Length 302;  
Best Local Similarity 46.3%; Pred. No. 6.3e-55;  
Matches 165; Conservative 48; Mismatches 80; Indels 63; Gaps 8;

QY 60 VMLIGRYDMRTTNLYLGSMAVSDLLILGLPFDLYLWRSRPVVGPELLCLSLYVCE 119  
Db 1 MLVWSRFREMRITTNLYLSSMAFSDLLIFLCMLDLFRLWQYRPNWNLGNLCKLFQFVSE 60  
QY 120 GCTYATLLHMTALSVERYLAIICRPLRARVLTTRRRVRLIAVLWAVALLSAGPFLFVGV 179  
Db 61 SCTYATVITITALSVERYFAICFPLRAKVVTGKRVKLVILVIMAVAFCSAGPIFVLGV 120  
QY 180 EQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAARAAALFSRECRPS- 238  
Db 121 EHD-----NGT-----DPRD-----TNECRATE 138  
QY 239 -PAQIGALRVMLWVTTAYFFLPFCLSLIYGLIGRELWSSRRPLRGPAASG---BERGHR 294  
Db 139 FAVRSGLLTVMVWSVFFFLFVCLTVLYSLIGRKLW---RRKRGAAVGSRLRDQNHK 195  
QY 295 QPKRVLLVVLAFIICWLPFHVGRITTY-----INTEDSRMMYFSQYENIVALQLFYLSASIN 351  
Db 196 QTVKMLAVVFAFICWLPFHVGRYLFKSLPFGSVETAQISQYCNLVSFVLFYLSAAN 255  
QY 352 PILYNLSKRYRAAFKLLLARKSRPRGFRHSRDTAGEVAGDTGGDTGYTETSAN 407  
Db 256 PILYNLSKRYRAVAVFVKLLGPFPFSQKRLSTLKDESSR-----AWTESSIN 301

Search completed: July 4, 2004, 03:16:30  
JOB time : 79 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 4, 2004, 03:07:32 ; Search time 28 Seconds  
(without alignments)  
1415.390 Million cell updates/sec

Title: US-09-876-252-130

Perfect score: 2156

Sequence: 1 MGSPWNGSDGPGAREPPWP.....DTGGDTVGVTYSANVKTMG 412

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	498	23.1	424	2 JH0164	neurotensin recept
2	491	22.8	418	2 S29506	neurotensin recept
3	451	20.9	477	2 JC7913	capa receptor (Cg)
4	434	20.1	418	2 A88013	Protein K10B4.4 [1
5	401	18.6	416	2 S68822	neurotensin recept
6	378	17.5	378	2 T15816	hypothetical prote
7	358	16.6	363	2 I57940	somatostatin recep
8	356.5	16.5	418	2 A46226	somatostatin recep
9	343	15.9	363	2 I57955	somatostatin recep
10	343	15.9	364	2 JN0763	somatostatin recep
11	342.5	15.9	380	2 AS2529	kappa opioid recep
12	338	15.7	352	2 JE0296	thyrotropin releas
13	338	15.7	380	2 S36143	kappa opioid recep
14	334	15.5	380	2 JC2338	kappa opioid recep
15	334	15.5	388	2 JN0605	somatostatin recep
16	333.5	15.5	367	2 I49022	kappa opioid recep
17	333.5	15.5	367	2 JC2421	opioid receptor ho
18	333.5	15.5	367	2 I56520	G protein-coupled
19	333.5	15.5	428	2 S30508	probable G protein
20	330.5	15.3	428	2 A44021	somatostatin recep
21	329.5	15.3	370	2 S43087	orphan opioid rece
22	328	15.2	380	2 A48227	kappa opioid recep
23	327	15.2	380	2 JC2434	kappa opioid recep
24	326.5	15.1	384	2 A47249	brain-specific som
25	325.5	15.1	372	2 I38532	delta opioid recep
26	321	14.9	384	2 J34629	somatostatin recep
27	320.5	14.9	372	2 S34592	delta opioid recep
28	320.5	14.9	398	2 JN0708	thyrotropin-releas
29	320	14.8	519	2 S17783	tachykinin recepto

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30      319      14.8      372      2      B48227      delta opioid recep
31      318.5      14.8      387      2      JC5949      galanin receptor 2
32      318      14.7      380      2      I38435      angiotensin recept
33      317      14.7      398      1      JQ1059      neurokinin 2 recep
34      317      14.7      411      2      I56444      thyrotropin-relea
35      317      14.7      412      2      S23436      thyroliberin recep
36      316      14.7      393      2      A39251      thyrotropin-releas
37      314      14.6      391      2      C41795      somatostatin recep
38      311      14.4      373      2      JE0087      delta opioid recep
39      311      14.4      384      1      S00516      neurokinin 2 recep
40      310      14.4      391      2      A39297      somatostatin recep
41      308.5      14.3      369      2      D41795      somatostatin recep
42      308.5      14.3      392      2      S65693      opioid receptor mu
43      308.5      14.3      400      2      I56553      mu opiate receptor
44      308      14.3      391      2      A41795      somatostatin recep
45      308      14.3      398      2      I56517      mu opioid receptor

```

## ALIGNMENTS

RESULT 1

JH0164

neurotensin receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 17-Mar-2000

C:Accession: JH0164

R:Tanaka, K.; Masu, M.; Nakanishi, S.

Neuron 4, 847-854, 1990

A:Title: Structure and functional expression of the cloned rat neurotensin receptor.

A:Reference number: JH0164; MUID:90297956; PMID:1694443

A:Accession: JH0164

A:Molecule type: mRNA

A:Residues: 1-424 <TAN>

C:Comment: Neurotensin receptor belongs to the family of G protein-coupled receptor. The  
ter (neurotensin) in the brain and as a hormone) cellular mediator in peripheral tis

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

F:65-87/Domain: transmembrane #status predicted <TM1>

F:97-121/Domain: transmembrane #status predicted <TM2>

F:144-165/Domain: transmembrane #status predicted <TM3>

F:189-210/Domain: transmembrane #status predicted <TM4>

F:236-260/Domain: transmembrane #status predicted <TM5>

F:309-330/Domain: transmembrane #status predicted <TM6>

F:348-372/Domain: transmembrane #status predicted <TM7>

F:4,38,42/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 23.1%; Score 498; DB 2; Length 424;

Matches 125; Conservative 58; Mismatches 111; Indels 86; Gaps 11;

QY 39 PVPTAVCLCLFVGVSGNVVTVMILGR---YRDMFTTNLYLGSMVSDLLI-LIGLPPD 94

Db 65 VLVTATYALFVGVGVGNSVTAFTLARKKSLQSLQSTVHYHLGSLSDLLILLAMPVE 124

QY 95 LYR-LWRGRPVVFGPLLCLSLYGVGEGCTYATLHMTALSVERYLAIQPLRVRVTR 153

Db 125 LYNFVWHVHPAFGADGCGYFFLRDACTYATLVNVALSVERYLAIQHPFKAKTMSRS 184

QY 154 RVRALIAVLNAVALISAGFFFLVGVGQDPGISVVPGLNGTARIASSPLASSPPLWLSRA 213

Db 185 RTKRFISALWLASALLAIPMLFTMGLQNSGDGTHFG-----GLVCTIVT----- 231

QY 214 PPPSPSPGPTAEAAALFSRECRPSPAQGLARVLMWTTAYFFL-PFLICSLYGLIGR 272

Db 232 -----ATVKVVIQVNTFMSFLFPMVLVILNTVIAN 262

QY 273 ELWSSRRRLRGPAAAGR-----EEGHRQTKR-----VLLVVVLAFLI 309

Db 263 KLTVM---VHQAEQGRVCTVGTGTHNGLEHSTFNMTIEPGRVQALRHGVLMRAVIAFW 319

QY 310 CWLPFPHVGRITTYINTEDSR---MMYFSQYFNIVALQFLYSASINPTLYNLISKYRAA 365

```
Db 320 CWLPYHVRRLMFCYISDEQWTFLEDFYHYFYLMTNALFVYSSAINPILNLYSANPRQV 379
QY 366 AFKLLLA-----RKSRP 377
Db 380 FLSTLACLCPGWRHRRKKRP 399

RESULT 2
S29506
neurotensin receptor - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-2000
C;Accession: S29506
P;Vita, N.; Laurent, P.; Lefort, S.; Chalon, P.; Dumont, X.; Kaghad, M.; Gully, D.; le F
FES Lett. 317, 139-142, 1993
A;Title: Cloning and expression of a complementary DNA encoding a high affinity human ne
A;Reference number: S29506; MUID:93154505; PMID:8381365
A;Accession: S29506
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-418 <VIT>
A;Cross-references: EMBL:X70070; NID:935020; PIDN:CAA49675.1; PID:935021
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 22.8%; Score 491; DB 2; Length 418;
Best Local Similarity 32.8%; Pred. No. 3.9e-32;
Matches 125; Conservative 62; Mismatches 118; Indels 76; Gaps 13;

QY 39 VPTAVCLCFVVGSGNVVTVMLIGR---YRDMRTTNLYLGSMAVSDLL-ILGLPFD 94
Db 64 VLTVAVTALFVVGTVGNTVTAFTLARKKLSQSLQSTVHYHLSGLSLLDILLAMPVE 123
QY 95 LYR-LWRSRPWFPGPLLRLSLVYGECTATLLHMTALSVRYLAICRPLRARVLVTRR 153
Db 124 LYNFIWVHPWAFGADGRCGYFLRDCTATALNVAASLSVERYLAICHFPKATLMSRS 183
QY 154 RVRAIALAVLWALLSAGPFLFLVGVBDPGISVVPGLNGTARIASSPLASPLWLSRA 213
Db 184 RTKFFISAIWLASALLTVMLFMWG-EQN----- 211
QY 214 PPPSPGPGTAPAAALFSRECRPSPAQGLRVLMLWVTT-AYFFLPFLCLSLYGLIGR 272
Db 212 -----RSADGQAGGLVCTPT-IHTATVKVVIQVNTFMSFIFPMVVISVLTIIAN 261
QY 273 ELWSSRPL--RCPAAS-----GREGRHQTKRVLLVVLAFICWLPFHV 316
Db 262 KLTWVRQAAGQGVCTVGEHSTFSAIEPGRVQALRHGVRVLRVAVVIAFVVCWLPYHV 321
QY 317 GRIIYINTEDSR---MMY-FSQYFNIVALQLFVLSASINPILNLYLSKKYR-----AA 365
Db 322 RRLMFCYISDEQWTFLEDFYHYFYMVTNALFVVSSTINPILNLYSANFRHIFLATLAC 381
QY 366 AFKLLIARKSRPRGFRHSRRT 386
Db 382 LCPVWRRRRKRP-AFSRKADS 401

RESULT 3
JC7913
capa receptor (CG14575) - fruit fly (Drosophila sp.)
C;Species: Drosophila sp.
C;Date: 31-Mar-2003 #sequence_revision 31-Mar-2003 #text_change 14-Jul-2003
C;Accession: JC7913
R;Iversen, A.; Cazzamali, G.; Williamson, M.; Hauser, F.; Grimmelikhuijzen, C.J.P.
Biochem. Biophys. Res. Commun. 299, 628-633, 2002
A;Title: Molecular cloning and functional expression of a Drosophila receptor for the ne
A;Reference number: JC7913; MUID:22347021; PMID:12459185
A;Accession: JC7913
A;Molecule type: mRNA
A;Residues: 1-477 <IVE>
A;Cross-references: GB:AF505865
C;Comment: This receptor that is a G-protein-coupled receptor stimulates renal (Malpighi
```

```
C;Genetics:
A;Introns: 70/3; 121/2; 126/1; 218/2; 276/2; 301/2; 349/1; 402/3; 436/3

Query Match 20.9%; Score 451; DB 2; Length 477;
Best Local Similarity 29.7%; Pred. No. 7.7e-29;
Matches 117; Conservative 68; Mismatches 135; Indels 74; Gaps 11;

QY 8 SDGPEGAREPPWPAALPPCDERRCSP-----FFLGAIVPVTVAVCLCLFVVGVSG 55
Db 30 SDPSHGFGBEDY----ACGTFCNSPKPEFVAFVLGPOTLPLYKAVLITITFGGIFITGVVG 85
QY 56 NVVTVMILIGRYDRMTTNLYLGSMAVSDLLILL-CLPFDLYRLWESRPWVFGPILCRLS 114
Db 86 NLIVCVIIRHSAMHTATNYIFLSAVSDLLYLLFGLTEVFLYWHQYFDLFGMPCKR 145
QY 115 LYVGECTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIALIWAVALLSAGPFL 174
Db 146 AFISEACTYVSFTIVAFSMERFLAICHPLHLVAMVGFKRAIRIITALMIVSFISAIPP- 204
QY 175 FLVGVQDPGISVVPGLNGTARIASSPLASPLWLSRAPPPSPGPETAEAALFSRE 234
Db 205 -----GLLSDIQYLNLYPLDHS-----RIEESAF----- 227
QY 235 CRPSPAQLGALRVMLWVTTAYTFPLPCLSLIYGLIGRELWSSRRPLRG--PAASGRERG 292
Db 228 CSMSPKIVNEIPVEVSFCIFVPMILILLYGRMGAKIRSNRTNOKLGVQOQTNNRSTR 297
QY 293 HRQTK-----RVLLVVVLAFLICWLPFHVGRIIYINTEDSRMVYFSQYFNI-----VAL 341
Db 288 NSQMRKKTIVIRMLAAVITFFVCWFFHLQRLIFLYAKN-----MDNYLDINEALFSIAG 342
QY 342 QLFLYSASINPILNLYLSKKYRAAFKLLIARKS 375
Db 343 FAYVSVCTVNPVIVYSMSRRYR-VAFRELLCGKA 375

RESULT 4
A88013
protein K10B4.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: A88013
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2016, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biologi
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.eleg
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: A88013
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-418 <STO>
A;Cross-references: GR:chr_II; PIDN:AB71009.1; PID:G2429475; GSPDB:GN000020; CESP:K10B4.4
A;Note: similar to family I of G-protein coupled receptors
C;Genetics:
A;Gene: K10B4.4
A;Map position: 2

Query Match 20.1%; Score 434; DB 2; Length 418;
Best Local Similarity 30.1%; Pred. No. 1.6e-27;
Matches 109; Conservative 77; Mismatches 138; Indels 38; Gaps 10;

QY 29 RGSPPFLGALVPVTVAVCLCFVVGSGNVVTVMLIGRYDRMTTNLYLGSMAVSDLL-I 87
Db 24 RCQ--SAGIVPTVIITYGTIFLLGFGNICTCIVTAANKSMNPTNYILFSLAVSDIAL 81
QY 88 LLGLPFDLYR-LWRSRPWFPGPLLCSLYVGECTYATLLHMTALSVERYLAICRPLRA 146
Db 82 ILGLPMEFYQSLDYSYPYRFSEGICKARAFLEFTSYASIMILICCFSEFRLAICHPLRS 141
QY 147 RVLVTRRRVRLIALIWAVALLSAGPFLFLVGVQDPP---GISVVEGLNGTARIASSP-A 203
Db 142 KIPFTLWRANVLIIALTWTISFCALPIATIVQINKLPLPEDAKYQPTNKNVFFVAVGVLN 201
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QY 204 SSPPLWLSRAPPSPSPGPTAAALRSREC-----RPSPAQLGALRVMLVWTTTAYFFL 258
Db 202 -----NRIFPV-----TDGIFVLHTEFCAMNQSRPDQOKM-----IIIFAFVTFVFI 244
QY 259 PFLCLISLYGLIGRELWSRRPLRGP--AASGREGRHQRKRVLLVAVLAFICWLPHVH 316
Db 245 PAIAIVIMYAHIAVLESEDDKGDQKVKRKNRNTLVKMLLSVVTFFICWLPFHI 304
QY 317 GRIIIVNTEDSRMMYFSYFNIVALQLFYL-----ASINPILYNLISKYRAAFKL 369
Db 305 QRLLSVYTTWSETTITISPPVQFLSMIVFISGFCYSYNSAANPILYNLISKYSAFCKT 364
QY 370 LL 371
Db 365 IL 366

RESULT 5
S68822
neurotensin receptor 2, leucobastine-sensitive - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 20-Jun-2000
C:Accession: S68822
R:Chalon, P.; Vita, N.; Kaghad, M.; Guillemot, M.; Bonnin, J.; Delpech, B.; le Fur, G.;
FEBS Lett. 386, 91-94, 1996
A:Title: Molecular cloning of a leucobastine-sensitive neurotensin binding site.
A:Reference number: S68822; MUID:96228041; PMID:8647296
A:Accession: S68822
A:Molecule type: mRNA
A:Residues: 1-416 <CHA>
A:Cross-references: GB:X97121; NID:g1483579; PIDN:CAA65787.1; PID:g1483580
A:Experimental source: hypothalamus
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
F:33-58/Domain: transmembrane #status predicted <TM1>
F:70-91/Domain: transmembrane #status predicted <TM2>
F:110-131/Domain: transmembrane #status predicted <TM3>
F:154-175/Domain: transmembrane #status predicted <TM4>
F:204-230/Domain: transmembrane #status predicted <TM5>
F:296-315/Domain: transmembrane #status predicted <TM6>
F:335-361/Domain: transmembrane #status predicted <TM7>

Query Match 18.6%; Score 401; DB 2; Length 416;
Best Local Similarity 29.4%; Pred. No. 7, 3e-25;
Matches 122; Conservative 68; Mismatches 145; Indels 80; Gaps 13;

QY 18 PWPALP-----PDERCSPPLGALVPVTAIVCLFVVGSGNVVMTMLIGRYDMRT 71
Db 6 PWPFRPSPSAGLSLEARGVDTLWAKVLTALYSLIFAFGTAGNALSVHVVVKARAGR 65
QY 72 -TTNLYLGSMVSDLLIL-GLPFDLYR-LWRSRPWVFGPLLCLRLSLVVGEGCTVATLH 128
Db 66 GLRLYHVLALSLALLLVLVSMPELYNFVWSHYVWFGDLGCRGYFVRELCAVATVLS 125
QY 129 MTALSVERLYAICPLRARVLVTRRRVALLAVLWALLSAGPFLFVLGV----- 179
Db 126 VASLSAERCLAVCQPLRARRLLTPRTRRLSLVWASLGALPMAVINGQKHEVESADG 185
QY 180 EQDPCISVVPGLNGTARIA-----SSPLASSPFLMLSRAPPSPSPGPTADAA 228
Db 186 EPEPASRVCTVLVSRATLQVFTQVNLVVSFALPLATLAF-----NGITVNLH 234
QY 229 ALFSRECRPSPAQLGALRVMLVWTTTAYFFLPLCLISLYGLIGRELWSRRPLRGPASG 288
Db 235 ALYS-QVFSAGAQSISPSRELGE-----EGLLGFTTWKTLUSLGVQASLV 281
QY 289 PERGHRQTK-----RVLLVVVLAFFICWLPHVGRITVNTED-----SRMMYFSQYENI 338
Db 282 RHKDAQSQRSLQHSQAVLRAIVAVVVCWLPVHAERLMYCYIPDDGTWNTLYDFHYFYM 341
QY 339 VALQFLYLSASINPILYNLISKYRAAFKLARKSRPRGFRHSRDTAGEVAGD 393
Db 339 VALQFLYLSASINPILYNLISKYRAAFKLARKSRPRGFRHSRDTAGEVAGD 393

Db 342 VNTLFFYVSSAVTPILYNNAVSSFR-----KULFL-----ESLGLSCGE 379

RESULT 6
TI5816
hypothetical protein C48C5.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Mar-2000
C:Accession: TI5816
R:Favell, A.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid C48C5.
A:Reference number: Z18410
A:Accession: TI5816
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-378 <FAV>
A:Cross-references: EMBL:U39994; NID:g1055102; PID:g1055105; PIDN:AAB37017.1; GSPDB:GNO(C
A:Experimental source: strain Bristol N2; clone C48C5
C:Genetics:
A:Gene: CESP:C48C5.1
A:Map position: X
A:Introns: 53/3; 87/2; 136/2; 169/3; 209/3; 231/3; 259/3; 286/1; 327/1
C:Superfamily: adenosine receptor A1

Query Match 17.5%; Score 378; DB 2; Length 378;
Best Local Similarity 28.7%; Pred. No. 4, 8e-23;
Matches 97; Conservative 70; Mismatches 135; Indels 36; Gaps 9;

QY 38 LVPVTAVCLCFVVGSGNVVTVMLIGRYDMRTTNLYLGSMVSDLLIL-LGPFEDLY 96
Db 51 LYKVTALYIFIFLGVGIVGNTTCLVMKHPMKTHASMYLMLNLAUSDVLTLCVGLPFEVM 110
QY 97 RLWRSRPWVFGPLLCLRLSLVVGEGCTVATLHMTALSVERLYAICRPL-RARVLVTRRV 155
Db 111 MNWQYPPWFPDYICNLKALIAETTSVSILTILFAIERVAVVCHPLFLMKVQPFKNI 170
QY 156 RALTAVLWAVALLSAGPFLFVLGVGEQDGISSVPGCLNGTARIASSPLASSPFLWLSRAPP 215
Db 171 GTIIGFTWIFSILCAMP--FAIHRADYIMKSWPQTDNRIPVKSMMCM----- 217
QY 216 PSPSPGPETAABAAALFSRECRPSPAQLGALRVML-VWTTAYFFLPLCLISLYGLIGREL 274
Db 218 -----IAYNF-----EPKLASTFKLPHFSAIAFFALPLFTIVILYARIACKV 260
QY 275 WSSRRPLRGPAAASGRGRHQRKRVLLVWVLAFFICWLPHVGRITVNTEDSRMM-YFS 333
Db 261 -SSNRTIQPGELDITEELQMRINAILCAIVSAFFICYLPQLRLFFYFDNEVILTVN 319
QY 334 QYFNIVALQLFYLGSINPILYNLISKYRAAFKL 371
Db 320 QYMFISGLFYLATIIINPIAYNLASSRFR-RAFKDIL 356

RESULT 7
I57940
somatostatin receptor 5 - rat
N:Alternate names: somatostatin release-inhibiting factor subtype 28 receptor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 24-Nov-1999
C:Accession: I57940; I57949; S39244
R:O'Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C.
Mol. Pharmacol. 42, 939-946, 1992
A:Title: Molecular cloning and expression of a pituitary somatostatin receptor with pref
A:Reference number: I57940; MUID:93125499; PMID:1362243
A:Accession: I57940
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-363 <OCAL>
A:Cross-references: GB:I04535; NID:g409238; PIDN:AAA17029.1; PID:g409239
R:O'Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C.
Mol. Pharmacol. 44, 1278, 1993
A:Title: Molecular cloning and expression of a pituitary somatostatin receptor with pref
```



A;Cross-references: GDB:119604; OMIM:182450  
 A;Map position: 3q28-3q28  
 C;Superfamily: vertebrate rhodopsin

Query Match 15.9%; Score 343; DB 2; Length 363;  
 Best Local Similarity 27.7%; Pred. No. 3.1e-20;  
 Matches 106; Conservative 58; Mismatches 131; Indels 88; Gaps 14;

QY 14 AREPPWALPP-----CDERR-CSPEP-LGA-----LVPVTAVCLCLFVVGSGNVTVM 62  
 DB 7 ASTPSWNASPGGAASGGDNRTLVPAPSAGARAVLPVLLVC--AAGLGGNTLIYV 64

QY 63 IGRYDRMTTNYLYGSMVSDLLILGLPDLRYLRWSPVFGPLLCRLSLYVGGCT 122  
 DB 65 VLRFKMTVTNYILNLAVADVLYMLGLPP-LATQNAASFMPGPGVLCRLVMTLDGVNQ 123

QY 123 YATLLHMTALSVRYLAICRPLRARVLTTRRRVALLAVLWAVALLSAGPFLFVGVQED 182  
 DB 124 FTSVFCITVMSVDRLAVVHPLSSARWRPRVAKLAGAAWVLSCLMSLPFLVADVQE- 182

QY 183 PGISVWPLGNTARIASSPLASPPMLSRAPPPSPGPETAFAAALFSRECRPSAQL 242  
 DB 183 -----GTCNAS-----W-----PEPVGL 196

QY 243 GALTVMWVTYAFPLPFLCLSLIYGLIGRELSSRRPLRGPASG-----RRGHRQT 296  
 DB 197 WGAFFIITVAVLGFAPLLVICLCYLLIVKV-----RAAGRVGCVRRSERKV 246

QY 297 KRVLVVVLAFFICWLPFHVGRIIYI-----NTEDSRMYFSQVFNIVALOLFYLASIN 351  
 DB 247 TRVLVVVLVFGWLPFFFTVINVLAVLPQEPASAGLYF---FVVI---LSYANSCAN 300

QY 352 PILYNIISKYRAAFAKLLARK 374  
 DB 301 PVLYGFLSDNFRSQFQVLCIRK 323

## RESULT 10

JN0763  
 somatostatin receptor 5 - human  
 C;Species: Homo sapiens (man)  
 C;Date: 30-Sep-1993 #sequence\_revision 20-Aug-1994 #text\_change 20-Jun-2000  
 C;Accession: JN0763  
 R;Yanada, Y.; Kagimoto, S.; Kubota, A.; Yasuda, K.; Masuda, K.; Someya, Y.; Ihara, Y.; I  
 Biochem. Biophys. Res. Commun. 195, 844-852, 1993  
 A;Title: Cloning, functional expression and pharmacological characterization of a fourth  
 A;Reference number: JN0762; MUID:93384611; PMID:8373420  
 A;Accession: JN0763  
 A;Molecule type: DNA  
 A;Residues: 1-364 <YAM>  
 A;Cross-references: DDBJ:D16827; NID:g487683; PIDN:BA04107.1; PID:g487684  
 C;Comment: This protein is a member of somatostatin receptor family.  
 C;Genetics:  
 A;Gene: GDB:SSTR5  
 A;Cross-references: GDB:138452; OMIM:182455  
 A;Map position: 16p13.3-16p13.3  
 A;Introns: #status absent  
 C;Superfamily: vertebrate rhodopsin  
 C;Keywords: G protein-coupled receptor; glycoprotein; lipoprotein; phosphoprotein; thiol  
 F;40-66/Domain: transmembrane #status predicted <TM1>  
 F;77-102/Domain: transmembrane #status predicted <TM2>  
 F;114-135/Domain: transmembrane #status predicted <TM3>  
 F;155-177/Domain: transmembrane #status predicted <TM4>  
 F;196-228/Domain: transmembrane #status predicted <TM5>  
 F;246-273/Domain: transmembrane #status predicted <TM6>  
 F;280-307/Domain: transmembrane #status predicted <TM7>  
 F;13,26,187/Binding site: carbohydrate (Aen) (covalent) #status predicted  
 F;112-186/Disulfide bonds: #status predicted  
 F;242,325/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status pred  
 F;247/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predic  
 F;320/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 15.9%; Score 343; DB 2; Length 364;

Best Local Similarity 27.7%; Pred. No. 3.1e-20;  
 Matches 106; Conservative 58; Mismatches 131; Indels 88; Gaps 14;

QY 14 AREPPWALPP-----CDERR-CSPEP-LGA-----LVPVTAVCLCLFVVGSGNVTVM 62  
 DB 7 ASTPSWNASPGGAASGGDNRTLVPAPSAGARAVLPVLLVC--AAGLGGNTLIYV 64

QY 63 IGRYDRMTTNYLYGSMVSDLLILGLPDLRYLRWSPVFGPLLCRLSLYVGGCT 122  
 DB 65 VLRFKMTVTNYILNLAVADVLYMLGLPP-LATQNAASFMPGPGVLCRLVMTLDGVNQ 123

QY 123 YATLLHMTALSVRYLAICRPLRARVLTTRRRVALLAVLWAVALLSAGPFLFVGVQED 182  
 DB 124 FTSVFCITVMSVDRLAVVHPLSSARWRPRVAKLAGAAWVLSCLMSLPFLVADVQE- 182

QY 183 PGISVWPLGNTARIASSPLASPPMLSRAPPPSPGPETAFAAALFSRECRPSAQL 242  
 DB 183 -----GTCNAS-----W-----PEPVGL 196

QY 243 GALTVMWVTYAFPLPFLCLSLIYGLIGRELSSRRPLRGPASG-----RRGHRQT 296  
 DB 197 WGAFFIITVAVLGFAPLLVICLCYLLIVKV-----RAAGRVGCVRRSERKV 246

QY 297 KRVLVVVLAFFICWLPFHVGRIIYI-----NTEDSRMYFSQVFNIVALOLFYLASIN 351  
 DB 247 TRVLVVVLVFGWLPFFFTVINVLAVLPQEPASAGLYF---FVVI---LSYANSCAN 300

QY 352 PILYNIISKYRAAFAKLLARK 374  
 DB 301 PVLYGFLSDNFRSQFQVLCIRK 323

## RESULT 11

A55259  
 kappa opioid receptor - guinea pig  
 N;Alternate names: dynorphin receptor  
 C;Species: Cavia porcellus (guinea pig)  
 C;Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 24-Nov-1999  
 C;Accession: A55259  
 R;Xie, G.; Meng, F.; Mansour, A.; Thompson, R.C.; Hoversten, M.T.; Goldstein, A.; Watson  
 Proc. Natl. Acad. Sci. U.S.A. 91, 3779-3783, 1994  
 A;Title: Primary structure and functional expression of a guinea pig kappa opioid (dynor  
 A;Reference number: A55259; MUID:94244825; PMID:8170987  
 A;Accession: A55259  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-380 <XTE>  
 A;Cross-references: GB:U04092; NID:g476106; PIDN:AAA67171.1; PID:g476107  
 C;Superfamily: vertebrate rhodopsin  
 C;Keywords: transmembrane protein

Query Match 15.9%; Score 342.5; DB 2; Length 380;  
 Best Local Similarity 25.1%; Pred. No. 3.6e-20;  
 Matches 102; Conservative 74; Mismatches 147; Indels 83; Gaps 12;

QY 2 GSPW-----NGSDGPEGAREPP---WPALPPCDERRCSPFPLGALVPVTAVCLCLF 49  
 DB 26 GSAWLPQAWPDGNGSAGPQDEQLEPAHISPAIP-----VIITAVYSVVF 70

QY 50 VVGSGNVVTVMILGRYDRMTTNYLYGSMVSDLLILGLPDLRYLRWSPVFGPL 109  
 DB 71 VVGLVGSNVFVIIRTKMTATNTNYIFNLADALVTTTTPFQ-STVIMNSWPEGDV 129

QY 110 LCRLSLYVGGCTYATLLHMTALSVRYLAICRPLRARVLTTRRRVALLAVLWAVALLS 169  
 DB 130 LCKIVISIDYNNFTSIFTLTMSVDRIYAVCHPVKALDFTPLKAKIINICILWSSSV 189

QY 170 AGPFLFVGVQEDPGISVWPLGNTARIASSPLASPPMLSRAPPPSPGPETAFAA 229  
 DB 190 GISAILLGGTKVREDVDIIE-----CSLQFPDDDDYSWD----- 223

QY 230 LFSRECRPSAQLGALTVMWVTYAFPLPFLCLSLIYGLIGRELSSRRPLRGPASGR 289







```
Query Match      15.5%; Score 334; DB 2; Length 388;
Best Local Similarity 26.9%; Pred.No.1.8e-19;
Matches 105; Conservative 65; Mismatches 128; Indels 92; Gaps 15;

Qy      1 MGSPW---NGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTAVCLCLFVVGVSGN 56
Db      15 LGTAWPSAANASSAPAEAE---AVAGFGDAR-----AAGWAIQCIYALVCLVGLVGN 65

Qy      57 VVTVMILGRYRDMKTTNNLYIGSMVSDLLILLGLPFDLYRLMRSRPWVFGPLLCRLSLY 116
Db      66 ALVIFVILRYAKMKTATNIYLLNLAVADELFMLSVPF-VASSAALRHWPFGSVLCRAVLS 124

Qy      117 VGEGETATLLHMTALSVERVLAICRPLRARVLTERR--VRALIIV-LMAVALLSAGPF 173
Db      125 VDGLNMFISVFCCLTVLSVDRIVAVVHPLRA---ATYRPSVAKLINLGWMLASLLTLP 181

Qy      174 LFLVGVQDFGISVVPGLNGTARIASSPLASSPPLMLSRAPPPSPSGPETAEAAALFSR 233
Db      182 AIFADTR-----PARGQA--VACNLQWHPAM-----SAVF-- 211

Qy      234 ECRSPAQLGALRVMLVTTAYFPLPCLLSILYGLIGREL-----WSSRRPLRGPA 285
Db      212 -----VVYFLLGFLPLVATGLCYLLIVGKRAVALRAGMQQR----- 251

Qy      286 ASGRERHROTGRVLLVVLAFIICWLPFHVGR--IVINTEDSRMMYFSCYENIVALQL 343
Db      252 -----RSEKKITRLVLMVVVVVFLCWMPFFVYVQLNLNVISLDATV-----NHVSLIL 299

Qy      344 FYLSASINPILYNLIISKYRAAFKLLAR 373
Db      300 SYANSCANPILYGFLSDNFRRSFORVLCRLR 329
```

Search completed: July 4, 2004, 03:10:54  
Job time : 29 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 3, 2004, 21:29:27 ; Search time 18 Seconds  
(without alignments)  
1191.828 Million cell updates/sec

Title: US-09-876-252-130

Perfect score: 2156

Sequence: 1 MGSPWNGSDGEGAREPPWP.....DTGGDTVGYTETSANVKTMG 412

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2149	99.7	412	1	MTLR_HUMAN
2	858.5	39.8	366	1	GHSR_PIG
3	857.5	39.8	366	1	GHSR_HUMAN
4	855.5	39.7	364	1	GHSR_RAT
5	614	28.5	257	1	GHSR_MOUSE
6	498	23.1	424	1	NTR1_RAT
7	495.5	23.0	424	1	NTR1_MOUSE
8	491	22.8	418	1	NTR1_HUMAN
9	451	20.9	477	1	CAPR_DROME
10	407	18.9	410	1	NTR2_HUMAN
11	404	18.7	417	1	NTR2_MOUSE
12	401	18.6	416	1	NTR2_RAT
13	369.5	17.1	362	1	SSR5_MOUSE
14	358	16.6	363	1	SSR5_RAT
15	355.5	16.5	418	1	SSR3_HUMAN
16	349.5	16.2	453	1	GP39_HUMAN
17	343	15.9	364	1	SSR5_HUMAN
18	342.5	15.9	380	1	OPRK_CAVPO
19	341.5	15.8	370	1	OPRK_CAVPO
20	338	15.7	380	1	OPRK_RAT
21	334	15.5	380	1	OPRK_HUMAN
22	334	15.5	388	1	SSR4_HUMAN
23	333.5	15.5	367	1	OPRK_MOUSE
24	333.5	15.5	367	1	OPRK_RAT
25	333.5	15.5	370	1	OPRK_PIG
26	333.5	15.5	428	1	SSR3_RAT
27	332.5	15.4	372	1	OPRD_HUMAN
28	331.5	15.4	395	1	TRFR_CHICK
29	331	15.4	372	1	GALS_RAT
30	330.5	15.3	428	1	SSR3_MOUSE
31	329.5	15.3	370	1	OPRK_HUMAN
32	328	15.2	380	1	OPRK_MOUSE
33	326.5	15.1	371	1	GALS_MOUSE

34	326.5	15.1	384	1	SSR4_RAT
35	323.5	15.0	370	1	GALT_RAT
36	321	14.9	384	1	SSR4_MOUSE
37	320.5	14.9	372	1	OPRD_RAT
38	320.5	14.9	398	1	TRFR_HUMAN
39	320	14.8	519	1	TLR2_DROME
40	319.5	14.8	368	1	OPRD_HUMAN
41	319	14.8	372	1	OPRD_MOUSE
42	319	14.8	453	1	CKKR_XENLA
43	318.5	14.8	387	1	GALS_HUMAN
44	318.5	14.8	398	1	TRFR_BOVIN
45	318	14.7	353	1	AFU_XENLA

P30937 rattus norv  
O88626 rattus norv  
P49660 mus musculu  
P33533 rattus norv  
P34981 homo sapien  
P30975 drosophila  
P60755 homo sapien  
P32300 mus musculu  
P70031 xenopus lae  
O43603 homo sapien  
O46639 bos taurus  
P79960 xenopus lae

#### ALIGNMENTS

RESULT 1  
MTLR\_HUMAN  
ID MTLR\_HUMAN STANDARD; PRT; 412 AA.  
AC O43193;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Motilin receptor (G protein-coupled receptor GPR38).  
GN GPR38 OR MTLR1 OR MTLR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM A).  
RX MEDLINE=98110578; PubMed=9441746;  
RA McKee K.K., Tan C.P., Palyha O.C., Liu J., Feighner S.D.,  
RA Hreniuk D.L., Smith R.G., Howard A.D., van der Ploeg L.H.T.;  
RT "Cloning and characterization of two human G protein-coupled receptor  
genes (GPR38 and GPR39) related to the growth hormone secretagogue  
and neuropeptide receptors.";  
RL Genomics 46:426-434 (1997).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).  
RX MEDLINE=9315084; PubMed=10381885;  
RA Feighner S.D., Tan C.P., McKee K.K., Palyha O.C., Hreniuk D.L.,  
RA Pong S.-S., Austin C.P., Figueroa D., MacNeil D., Cascieri M.A.,  
RA Nargund R., Bakshi R., Abramovitz M., Stocco R., Kargman S.,  
RA O'Neill G., van Der Ploeg L.H.T., Evans J., Patchett A.A., Smith R.G.,  
RA Howard A.D.;  
RT "Receptor for motilin identified in the human gastrointestinal  
system.";  
RL Science 284:2184-2188 (1999).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM A).  
RX Wall M.;  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP FUNCTION.  
RX MEDLINE=21219832; PubMed=11325507;  
RA Smith R.G., Leonard R., Bailey A.R.T., Palyha O.C., Feighner S.D.,  
RA Tan C.P., McKee K.K., Pong S.-S., Griffin P.R., Howard A.D.;  
RT "Growth hormone secretagogue receptor family members and ligands.";  
RL Endocrine 14:9-14 (2001).  
CC -!- FUNCTION: Receptor for motilin.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=A;  
CC IsoId=O43193-1; Sequence=Displayed;  
CC Name=B;  
CC IsoId=O43193-2; Sequence=VSP\_001894;  
CC -!- TISSUE SPECIFICITY: Expressed only in thyroid, stomach, and bone  
marrow.  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
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CC EMBL; AF034632; AAC26081.1; -;  
 DR EMBL; AL137000; CAC19107.1; -;  
 DR Genew; HGNC:4495; GPR38.  
 DR MIM; 602885; -;  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.  
 DR GO; GO:0007586; P:digestion; TAS.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1\_1; 1.  
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Alternative splicing.

FT DOMAIN 1 35 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 36 56 1 (POTENTIAL).  
 FT DOMAIN 57 74 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 75 94 2 (POTENTIAL).  
 FT DOMAIN 95 112 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 113 134 3 (POTENTIAL).  
 FT DOMAIN 135 157 4 (POTENTIAL).  
 FT TRANSMEM 158 178 5 (POTENTIAL).  
 FT DOMAIN 179 246 6 (POTENTIAL).  
 FT TRANSMEM 247 270 7 (POTENTIAL).  
 FT DOMAIN 271 298 8 (POTENTIAL).  
 FT TRANSMEM 299 320 9 (POTENTIAL).  
 FT DOMAIN 321 334 10 (POTENTIAL).  
 FT TRANSMEM 335 358 11 (POTENTIAL).  
 FT DOMAIN 359 412 12 (POTENTIAL).  
 FT TRANSMEM 413 412 13 (POTENTIAL).  
 FT BY SIMILARITY.  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT QLVVLAFLICWLPFHVGRILIIYNTEDSRMMYFSQYFNIVAL  
 FT LQVLSINPILYLNLSKKYRAAFKLLARKSRPRGFR  
 FT SRDTAGEVAGTGDVTGYTETSANVKTWG -> RKWSRRG  
 FT SKDACLOSAPGTAQTGLPLLAQLAPLPAPPEISIPAS  
 FT TRGGSGIYNLVALPRWQNLHKGFRFADVLLSVL  
 FT (in isoform B).  
 FT /FTID=VSP\_001894.  
 SQ SEQUENCE 412 AA; 45344 MW; CL3FF6165012DEF3 CRC64;

Query Match 99.7%; Score 2149; DB 1; Length 412;  
 Best Local Similarity 99.8%; Pred. No. 6.3e-135;  
 Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGPEGAREPPALPCDERRCPPLGALVPTAVCLCFVVGSGNVTV 60  
 Db 1 MGSPWNGSDGPEGAREPPALPCDERRCPPLGALVPTAVCLCFVVGSGNVTV 60  
 QY 61 MLIGRVDMRTTNLYLGSMAVSDLLILGLPDLRLMSRWVWVGLLCRLSLVYVGE 120  
 Db 61 MLIGRVDMRTTNLYLGSMAVSDLLILGLPDLRLMSRWVWVGLLCRLSLVYVGE 120  
 QY 121 CTYATLLHMTALSVRYLAICRLRLARVLVTRVRVALIAVLWAVALLSAGPFLVGVGE 180  
 Db 121 CTYATLLHMTALSVRYLAICRLRLARVLVTRVRVALIAVLWAVALLSAGPFLVGVGE 180  
 QY 181 QDPGISVWFLNGTARIASPLASSPPLMLSRAPPSPGPGTAAALFSRECRPSA 240  
 Db 181 QDPGISVWFLNGTARIASPLASSPPLMLSRAPPSPGPGTAAALFSRECRPSA 240  
 QY 241 QLGLARVLMVWTTAYFFLPCLLSILYGLIGRLWSRRPLRGPASGRGRHQVRL 300  
 Db 241 QLGLARVLMVWTTAYFFLPCLLSILYGLIGRLWSRRPLRGPASGRGRHQVRL 300

QY 301 LVVLAFLICWLPFHVGRILIIYNTEDSRMMYFSQYFNIVALQFLYLSASINPILNLSK 360  
 Db 301 LVVLAFLICWLPFHVGRILIIYNTEDSRMMYFSQYFNIVALQFLYLSASINPILNLSK 360  
 QY 361 KYRAAFAKLLARKSRPRGFRSRDTAGEVAGTGDVTGYTETSANVKTWG 412  
 Db 361 KYRAAFAKLLARKSRPRGFRSRDTAGEVAGTGDVTGYTETSANVKTWG 412

# RESULT 2

## GHSR\_PIG

ID GHSR\_PIG STANDARD; PRT; 366 AA.  
 AC Q95254; Q95255;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Growth hormone secretagogue receptor type 1 (GHS-R) (GH-releasing  
 DE peptide receptor) (GHRP) (Ghrelin receptor).  
 GN GHSR.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).  
 RC STRAIN=Yorkshire; TISSUE=Pituitary;  
 RX MEDLINE=96337998; PubMed=8688086;  
 RA Howard A.D., Feighner S.D., Cully D.F., Arena J.P.,  
 RA Liberator P.A., Rosenblum C.I., Hamelin M., Hreniuk D.L., Liu X.K.,  
 RA Palaya O.C., Anderson J., Paress P.S., Diaz C., Chou M., Liu X.K.,  
 RA McKee K.K., Pong S.-S., Chaug L.-Y., Elbrecht A., Dashkevich M.,  
 RA Heavens R., Rigby M., Sirinathsinghji D.J.S., Dean D.C., Melillo D.G.,  
 RA Patchett A.A., Nargund R., Griffin P.R., Demartino J.A., Gupta S.K.,  
 RA Schaeffer J.M., Smith R.G., van der Ploeg L.H.F.;  
 RA "A receptor in pituitary and hypothalamus that functions in growth  
 RT hormone release.";  
 RL Science 273:974-977(1996).  
 CC -!- FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins.  
 CC Stimulates growth hormone secretion. Binds also other growth  
 CC hormone releasing peptides (GHRP) (e.g. Met-enkephalin and GHRP-6)  
 CC as well as non-peptide, low molecular weight secretagogues (e.g.  
 CC 1-692,429, MK-0677, adenosine).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Name=1A;  
 CC IsoId=Q95254-1; Sequence=Displayed;  
 CC Name=1B;  
 CC IsoId=Q95254-2; Sequence=VSP\_001918, VSP\_001919;  
 CC -!- TISSUE SPECIFICITY: Pituitary and hypothalamus.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; U60178; AAC48630.1; -;  
 DR EMBL; U60180; AAC48631.1; -;  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN  
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1\_1; 1.  
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Alternative splicing.  
 FT DOMAIN 1 40 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 41 66 1 (POTENTIAL).  
 FT DOMAIN 67 72 CYTOPLASMIC (POTENTIAL).

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FT TRANSMEM 73 96 2 (POTENTIAL).
FT DOMAIN 97 117 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 118 139 3 (POTENTIAL).
FT DOMAIN 140 162 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 163 183 4 (POTENTIAL).
FT DOMAIN 184 211 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 212 235 5 (POTENTIAL).
FT DOMAIN 236 263 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 264 285 6 (POTENTIAL).
FT DOMAIN 286 302 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 303 326 7 (POTENTIAL).
FT DOMAIN 327 366 CYTOPLASMIC (POTENTIAL).
FT DISULFID 116 198 BV SIMILARITY.
FT CARBOHYD 13 13 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 266 289 AVVFAPILCWLPFHVGRYLFSSK -> GSGQCALRLSLPG
/PLHSSCLFSP (in isoform 1B).
/FTID-VSP 001918.
Missing (in isoform 1B).
/FTID-VSP 001919.
FT VARGPLIC 290 366
SEQUENCE 366 AA; 41194 MH; 2C850B3EF61B7C1C CRC64;
Query Match 39.8%; Score 858.5; DB 1; Length 366;
Best Local Similarity 44.9%; Pred. No. 6.8e-50;
Matches 188; Conservative 55; Mismatches 105; Indels 71; Gaps 10;
QY 5 WNGSDGPEGA-----REPPWALPPCD-----ERRCSPPFPGALVPVTVAVCLCLFVVGVSQN 56
Db 2 WNAFSEEPGNLTLPDLGWDAPPENDSLVEELLPLFTPLLAGVTATCVALLFVVGIA 61
QY 57 VVTVMILIGRYDMRTTNLYLGSMAVSDLLILLGLPDLVRLWRSRPWVFGPLCLSLSY 116
Db 62 LITMLVSEFREMRTTNLYLSMAFSDLLIFCLMDLDFRLWQRPWMLGNLCKLPF 121
QY 117 VQEGCTATLLHWTALSVERYLAICRPLARVLTERRRVRALIAVLAVALLSAGPLFL 176
Db 122 VSESCYATVLTITALSVERYFAICFPLRAKVVKGRVQLVILVIAVAFCSAGPIFVL 181
QY 177 VGVEODPGISVVGNGIATARIASSPLASSPPLWLRAPPPSPSPETAALFSSRCR 236
Db 182 VGVEHD-----NGT-----DPRD-----TNECR 199
QY 237 PS--PAQLGALRVMLVWTTAYTFPLPCLSLYGLIGRELSSRPLRGPASG---RER 291
Db 200 ATEPAVRSLTVMVWVSFFFLPVCLTVLSILGRKLW---RRKGEAVGSLRDQ 256
QY 292 GHRQTKRVLLVVLAFITICWLPFHVGRYIY---INTEDSRMVFYSQYFNIVALQLFYLSA 348
Db 257 NHKQTKRVMLVWVFAFICWLPFHVGRVLFSSKLEPGSVIEIAIQISQYCNLVSVFLFYLSA 316
QY 349 SINPTLYNLISKYRAAFAKLLARKSPRGHRSRDTAGEVAGTGDGTGYTTSAN 407
Db 317 AINPLIYNIMSKYRAVAVFKLGLGFPFQSKLSTLKDESSR-----AWTESSIN 365

RESULT 3
GHSR HUMAN
ID GHSR HUMAN STANDARD; PRT; 366 AA.
AC Q92847; Q92848; Q96R77;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-MAR-2004 (Rel. 35, Last sequence update)
DE Growth hormone secretagogue receptor type 1 (GHS-R) (GH-releasing
peptide receptor) (GHRP) (Ghrelin receptor).
GN GHSR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]_
RN SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).
RC TISSUE=Pituitary;
RX MEDLINE=96337998; PubMed=8668086;

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RA Howard A.D., Feighner S.D., Cully D.F., Arena J.P.,
RA Liberator P.A., Rosenblum C.I., Hamelin M., Hreniuk D.L.,
RA Palyha O.C., Anderson J., Parese P.S., Diaz C., Chou M., Liu K.K.,
RA McKee K.K., Pong S.-S., Chaung L.-Y., Elbrecht A., Dashkevicz M.,
RA Heavens R., Rigby M., Sirinathsinghji D.J.S., Dean D.C., Melillo D.G.,
RA Patchett A.A., Nargund R., Griffin P.R., Demartino J.A., Gupta S.K.,
RA Schaeffer J.M., Smith R.G., van der Ploeg L.H.T.;
RA "A receptor in pituitary and hypothalamus that functions in growth
RT hormone release.";
RT Science 273:974-977 (1996).
RN [2]
RN SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).
RP MEDLINE=21255649; PubMed=11356716;
RX Petersenn S., Rasch A.C., Pershonn M., Beil F.U., Schulte H.M.;
RT "Genomic structure and transcriptional regulation of the human growth
RT hormone secretagogue receptor";
RT Endocrinology 142:2649-2659 (2001).
RN [3]
RN SEQUENCE FROM N.A. (ISOFORM 1B).
RP Kopatz S.A., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RN FUNCTION.
RP MEDLINE=21219832; PubMed=11322507;
RX Smith R.G., Leonard R., Bailey A.R.T., Palyha O.C., Feighner S.D.,
RA Tan C.P., McKee K.K., Pong S.-S., Griffin P.R., Howard A.D.;
RT "Growth hormone secretagogue receptor family members and ligands.";
RL Endocrine 14:9-14 (2001).
RN [5]
RN FUNCTION.
RP MEDLINE=20067959; PubMed=10604470;
RX Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
RT "Ghrelin is a growth-hormone-releasing acylated peptide from
RT stomach.";
RL Nature 402:656-660 (1999).
CC -!- FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins.
CC Stimulates growth hormone secretion. Binds also other growth
CC hormone releasing peptides (GHRP) (e.g. Met-enkephalin and GHRP-6)
CC as well as non-peptide, low molecular weight secretagogues (e.g.
CC L-692,429, MK-0677, adenosine).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1A;
CC IsoId=Q92847-1; Sequence=Displayed;
CC Name=1B;
CC IsoId=Q92847-2; Sequence=VSP_001916, VSP_001917;
CC -!- TISSUE SPECIFICITY: Pituitary and hypothalamus.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; U60179; AAC50653.1; -.
CC EMBL; U60181; AAC50654.1; -.
CC EMBL; AF369786; AAK71539.1; -.
CC EMBL; AF369786; AAK71540.1; -.
CC EMBL; AY322544; AAP84357.1; -.
CC Genew; HGNC:4267; GHSR.
CC MIM; 601898; -.
CC GO; GO:0016021; C:integral to membrane; TAS.
CC GO; GO:0005886; C:plasma membrane; TAS.
CC GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.

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DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G PROTEIN RECP Fl 1; 1.
DR PROSITE; PS00262; G PROTEIN RECP Fl 2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Alternative splicing.
FT DOMAIN 1 40 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 41 66 1 (POTENTIAL).
FT DOMAIN 67 72 2 (POTENTIAL).
FT TRANSMEM 73 96 2 (POTENTIAL).
FT DOMAIN 97 117 3 (POTENTIAL).
FT TRANSMEM 118 139 3 (POTENTIAL).
FT DOMAIN 140 162 4 (POTENTIAL).
FT TRANSMEM 163 183 4 (POTENTIAL).
FT DOMAIN 184 211 5 (POTENTIAL).
FT TRANSMEM 212 235 5 (POTENTIAL).
FT DOMAIN 236 264 6 (POTENTIAL).
FT TRANSMEM 265 302 6 (POTENTIAL).
FT DOMAIN 303 326 7 (POTENTIAL).
FT TRANSMEM 327 366 7 (POTENTIAL).
FT DISULFID 116 198 BY SIMILARITY.
FT CARBOHYD 13 13 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 27 27 N-LINKED (GLCNAC... ) (POTENTIAL).
FT VARSPLIC 266 289 AVVAFILCMLPFHVGRLYFSSK -> GGSQALRLSLAG
PILSLCLPFL (in isoform 1B).
FTID=VSP 001916.
FTID=VSP 001917.
FT VARSPLIC 290 366 Missing (in isoform 1B).
FTID=VSP 001917.
FT VARSPLIC 366 AA; 41328 MW; D1862710DA9DC0C6 CRC64;
SQ SEQUENCE 366 AA; 41328 MW; D1862710DA9DC0C6 CRC64;

Query Match 39.8%; Score 857.5; DB 1; Length 366;
Best Local Similarity 44.5%; Pred. No. 7.9e-50;
Matches 185; Conservative 59; Mismatches 107; Indels 65; Gaps 9;

QY 5 WNGSDGPEGA-----REPPWALPCD---ERRCSPPFLGALVPVTVAVCLCLFVVGSGN 56
DQ 2 WNAFSEBPGNLTADLDWDASPGNDSLGDELQLQFPAPLAGVATCATVAFVVGAGN 61
QY 57 VVTWMLIGRYDMRTTNTLYLGSMAVSDLLILLGLPFLYRLWRSRPWVGFLPCLRLSLY 116
DQ 62 LLTLMVSVRPRELRTTNTLYLSSMAFSDLLIFLCMLDVLWQYRPNWGDLLCKLQFQF 121
QY 117 VEGCTATLHMTALSVERVYLCRPLARVLTTRRRVRLIAVLMAVALLSAGFLFL 176
DQ 122 VSECTATVTTITALSVERVYLCFPLARVTKGVKLVIFVIWAVAFCSAGPIFVL 181
QY 177 VGVQDPGIVSVVGLNGTARIASSPLSLSRAPPSPSPGSPETAFAAALFSRECR 236
DQ 182 VGVBE-----NGT-----DP--W-----DTNECR 199
QY 237 PS--PAQIGALRVLWVTAYFFFLCLSLYGLIGRELWSSRRPLRGPAAQRGRGHR 294
DQ 200 PTEFAVRSGLLTVMVWSSIFFFLPVFLCLTVLSLIGKLRWRGDAVVGASLRDQNHK 259
QY 295 QTKRVLVWVLAFTICMLPHVGRILINTEDS---RMVFSQVFNIVALQLFYLSASIN 351
DQ 260 QTVKLVAVVFAFLCMLPHVGRVYFSKSPFGSLIEAQISQCNLVSVFLYLSAAN 319
QY 352 PILYNLSKRYAAAFKLLARKSRPRGFRHSRDTAGEVAGDTGGDTVGVTETSAN 407
DQ 320 PILYNMSKKYRVAVFLGLGFEFSSQKSLTLKDESR-----AWTESSIN 365

RESULT 4
GHSR RAT STANDARD; PRT; 364 AA.
AC 008725;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, last sequence update)
DT 28-FEB-2003 (Rel. 41, last annotation update)
DE Growth hormone secretagogue receptor type 1 (GHS-R) (GH-releasing
DE peptide receptor) (GHRP) (Ghrelin receptor).
GN GHSR.

```

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OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]_TaxId=10116;
RP SEQUENCE FROM N.A.
RT TISSUE=pituitary;
RX MEDLINE=97246555; PubMed=9092793;
RA McKee K.K., Palyha O.C., Feighner S.D., Hreniuk D.L., Tan C.P.,
RA Phillips M.S., Smith R.G., der Ploeg L.H.F., Howard A.D.;
RT "Molecular analysis of rat pituitary and hypothalamic growth hormone
RT secretagogue receptors.";
RL Mol. Endocrinol. 11:415-423 (1997).
RN [2]
RP SEQUENCE OF 1-240 FROM N.A.
RT STRAIN=Wistar; TISSUE=pituitary;
RX MEDLINE=98100386; PubMed=9437732;
RA Yokote R., Sato M., Matsubara S., Ohye H., Niimi M., Murao K.,
RA Takahara J.;
RT "Molecular cloning and gene expression of growth hormone-releasing
RT peptide receptor in rat tissues.";
RL Peptides 19:15-20 (1998).
RN [3]
RP FUNCTION
RX MEDLINE=20067959; PubMed=10604470;
RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
RT "Ghrelin is a growth-hormone-releasing acylated peptide from
RT stomach.";
RL Nature 402:656-660 (1999).
CC -!- FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins.
CC Stimulates growth hormone secretion. Binds also other growth
CC hormone releasing peptides (GHRP) (e.g. Met-enkephalin and GHRP-6)
CC as well as non-peptide, low molecular weight secretagogues (e.g.
CC L-692,429, MK-0677, adenosine) (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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EMBL; U94321; AAC53156.1; --
EMBL; AB001982; BAA21777.1; ALT INIT.
InterPro; IPR000276; GPCR_Rhodopsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRHHODOPS.
PROSITE; PS00237; G PROTEIN RECP Fl 1; 1.
PROSITE; PS00262; G PROTEIN RECP Fl 2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 40 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 41 66 1 (POTENTIAL).
FT DOMAIN 67 72 2 (POTENTIAL).
FT TRANSMEM 73 96 2 (POTENTIAL).
FT DOMAIN 97 117 3 (POTENTIAL).
FT TRANSMEM 118 139 3 (POTENTIAL).
FT DOMAIN 140 162 4 (POTENTIAL).
FT TRANSMEM 163 183 4 (POTENTIAL).
FT DOMAIN 184 211 5 (POTENTIAL).
FT TRANSMEM 212 235 5 (POTENTIAL).
FT DOMAIN 236 264 6 (POTENTIAL).
FT TRANSMEM 265 302 6 (POTENTIAL).
FT DOMAIN 303 326 7 (POTENTIAL).
FT TRANSMEM 327 364 7 (POTENTIAL).
FT DISULFID 115 197 BY SIMILARITY.
FT CARBOHYD 13 13 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 26 26 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 364 AA; 40963 MW; DC3F559BB061EE9 CRC64;

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Query Match 39.7%; Score 855.5; DB 1; Length 364;  
 Best Local Similarity 48.0%; Pred. No. 1.1e-49;  
 Matches 184; Conservative 52; Mismatches 82; Indels 65; Gaps 11;

QY 5 WNGSDGPGAREP-----PWPALPPCD---ERRCSPPFLGALVPTAVCLCLFVVGVS 55  
 Db 2 WNAT--PSEEPENVTLDWDASPGNDSLDPDELLFPAPLLAGVTATCVAFVVGIS 59

QY 56 NVVTMLIGRYDMRTTNLYLGSMAVSDLLILGLPFDLYLWRSRPVVGPLCLLSL 115  
 Db 60 NLLTMLVSRFRRLTTNLYLSSMAFSDLLIFLCPDLVRLWQYRPNWFGDLCKLFQ 119

QY 116 YVGECTVATLHMTALSVERYLACRPLRVLVTRRRVRLALVAVALLSAGPPLF 175  
 Db 120 FVSECTVATLITLALSVERYFAICFPLRAKVVTGKVKLVILVAVAFCSAGPIFV 179

QY 176 LVGVEQDPCISVVGPGINGTARTASSPLSLWRAPPPSPGPTABAAALFREC 235  
 Db 180 LVGVEHE-----NGT-----DPRD-----TNEC 197

QY 236 RPS--PAQGLRVLMTVTTAYFFFLCLSLYGLIGELWSSRRPLRGPAASG---RE 290  
 Db 198 RATEFAVRSGLLTVMVWSSVFFFLVCLTVLSLIGRKLW--RR--RGDAVVGSSURD 253

QY 291 RGHRTKRLVLLVLAIIICWLPVHGRYIINTEDS---RMVFYSQYFNIVALQLFYL 347  
 Db 254 QNHQTVKMLAVVVFAPILCWLPHVGRYLFKSPFGSLFELIAQISQYCNLVSVFLYL 313

QY 348 ASINPILYLNLSKKYRAAFKLL 370  
 Db 314 AAINPILYLNLSKKYRVAVFKLL 336

RESULT 5  
 GHRS MOUSE  
 ID GHRS MOUSE STANDARD; PRT; 257 AA.  
 AC Q99P50; Q91Z82;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Growth hormone secretagogue receptor type 1 (GHS-R) (GH-releasing peptide receptor) (GHRP) (Ghrelin receptor) (Fragment).  
 GN GHRS.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE OF 1-183 FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;  
 RA Kacsch B.;  
 RT "Cloning of mouse ghrelin/growth hormone secretagogue receptor cDNA by rapid amplification of cDNA ends (RACE).";  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 73-257 FROM N.A.  
 RC STRAIN=129S3/SvImJ;  
 RA Peng X., Frohman L.A., Kineman R.D.;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins. Stimulates growth hormone secretion. Binds also other growth hormone releasing peptides (GHRP) (e.g. Met-enkephalin and GHRP-6) as well as non-peptide, low molecular weight secretagogues (e.g. L-692,429, MK-0677, adenosine) (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC -----  
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CC EMBL; AY056474; AAL13336.1; --  
 CC EMBL; AF332997; AAG61141.1; --  
 DR InterPro; IPR000276; GPCR Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G-PROTEIN RECP\_F1\_1; 1.  
 DR PROSITE; PS0262; G-PROTEIN RECP\_F2\_1;  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.  
 FT DOMAIN 1 35  
 FT EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 36 58  
 FT DOMAIN 59 77  
 FT TRANSMEM 78 100  
 FT DOMAIN 101 125  
 FT TRANSMEM 126 148  
 FT DOMAIN 149 160  
 FT TRANSMEM 161 183  
 FT DOMAIN 184 211  
 FT TRANSMEM 212 234  
 FT DOMAIN 235 257  
 FT DISULFID 115 197  
 FT CARBOHYD 13 13  
 FT CARBOHYD 26 26  
 FT CARBOHYD 187 187  
 FT NON TER 257 257  
 SQ SEQUENCE 257 AA; D6FA21EAB0E30791 CRC64;

Query Match 28.5%; Score 614; DB 1; Length 257;  
 Best Local Similarity 45.1%; Pred. No. 6.4e-34;  
 Matches 137; Conservative 39; Mismatches 66; Indels 62; Gaps 10;

QY 5 WNGSDGPGAREP-----PWPALPPCD---ERRCSPPFLGALVPTAVCLCLFVVGVS 55  
 Db 2 WNAT--PSEEPENVTLDWDASPGNDSLDPDELLFPAPLLAGVTATCVAFVVGIS 59

QY 56 NVVTMLIGRYDMRTTNLYLGSMAVSDLLILGLPFDLYLWRSRPVVGPLCLLSL 115  
 Db 60 NLLTMLVSRFRRLTTNLYLSSMAFSDLLIFLCPDLVRLWQYRPNWFGDLCKLFQ 119

QY 116 YVGECTVATLHMTALSVERYLACRPLRVLVTRRRVRLALVAVALLSAGPPLF 175  
 Db 120 FVSECTVATLITLALSVERYFAICFPLRAKVVTGKVKLVILVAVAFCSAGPIFV 179

QY 176 LVGVEQDPCISVVGPGINGTARTASSPLSLWRAPPPSPGPTABAAALFREC 235  
 Db 180 LVGVEHE-----NGT-----DPRD-----TNEC 197

QY 236 RPS--PAQGLRVLMTVTTAYFFFLCLSLYGLIGELWSSRRPLRGPAASG---RE 290  
 Db 198 RATEFAVRSGLLTVMVWSSVFFFLVCLTVLSLIGRKLW--RR--RGDAVVGSSURD 253

QY 291 RGHRTKRLVLLVLAIIICWLPVHGRYIINTEDS---RMVFYSQYFNIVALQLFYL 347  
 Db 254 QNHQTVKMLAVVVFAPILCWLPHVGRYLFKSPFGSLFELIAQISQYCNLVSVFLYL 313

RESULT 6  
 NTRI RAT  
 ID NTRI RAT STANDARD; PRT; 424 AA.  
 AC P20789;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Neurotensin receptor type 1 (NTR-1) (High-affinity leucobastine-insensitive neurotensin receptor) (NTRH).  
 DE NTSR1.  
 GN Rattus norvegicus (Rat).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.



RC TISSUE=Brain;  
 RA MEDLINE=90297956; PubMed=1694443;  
 RX Tanaka K., Masu M., Nakanishi S.;  
 RT "Structure and functional expression of the cloned rat neurotensin  
 receptor.";  
 RL Neuron 4:847-854(1990).  
 CC -1- FUNCTION: Receptor for the tridecapeptide neurotensin. It is  
 associated with G proteins that activate a phosphatidylinositol-  
 calcium second messenger system.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC Highest to tachykinins receptors.  
 DR PTR; JH0164; JH0164.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR InterPro; IPR003985; NT1\_Receptor.  
 DR InterPro; IPR003984; NT1\_Receptor.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODOPSN.  
 DR PRINTS; PR01479; NEUROTENSINR.  
 DR PRINTS; PR01480; NEUROTENSINR.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Phosphorylation; Lipoprotein; Palmitate.  
 FT DOMAIN 1 64  
 FT TRANSMEM 65 87  
 FT DOMAIN 88 96  
 FT CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 97 121  
 FT DOMAIN 122 143  
 FT TRANSMEM 144 165  
 FT DOMAIN 166 188  
 FT TRANSMEM 189 210  
 FT DOMAIN 211 235  
 FT TRANSMEM 236 260  
 FT DOMAIN 261 308  
 FT TRANSMEM 309 330  
 FT DOMAIN 331 348  
 FT TRANSMEM 349 372  
 FT DOMAIN 373 424  
 FT CYTOPLASMIC (POTENTIAL).  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 38 38  
 FT CARBOHYD 42 42  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT DISULFID 142 225  
 FT LIPID 388 388  
 FT S-palmitoyl cysteine (Potential).  
 SQ SEQUENCE 424 AA; 47054 MW; A9C2F7EAF8D9BCD3 CRC64;

Query Match  
 Best Local Similarity 23.1%; Score 498; DB 1; Length 424;  
 Matches 125; Conservative 58; Mismatches 111; Indels 86; Gaps 11;  
 39 VPVTAVCLCLFVVGVSGNVVTVMLIGR---YRDMRTTNLYLGSMAVSDLLI-LLGLPFD 94  
 65 VLVTAYIALFVVGTVGNSVATLARKKSLSQSTVHVHLSLSLSDLLILLAMPVE 124  
 95 LYR-LNRSRPWPGPLLCRLSLYVGECTVATLHMTALSVRYLAICRPLRAVLVTRR 153  
 125 LYNFIWVHPWAFGDAGCGRYFLRDCTVATNALNVASLSVERLYLAICHPFKAKTLMRS 184  
 154 RVKALLAVLWAVALLSAGPFLVLGVGQDPGISVVPGLNLTARIASPLASSPFLWLSRA 213  
 185 RTKFKFSAILWASALLAIPMLFTMGQNRSGDTHPG-----GLVCTPIVDT----- 231  
 214 PFPSPSPGPTAEAAALFSRECRPSPAQLGALRVMLVWTTAYFFL-PFLCLSLYLGLIGR 272  
 232 -----ATVKVQVNTFMFLPMLVISLNVIAN 262  
 273 ELWSSRRPLRGPASGR-----ERHQRQTKR-----VLLVWVLAFLII 309  
 263 KLTWM---VHQAAEQGRVCTVGTNGHLESTFNMTIEPGRVQALRHGVILVRAVIAFVV 319  
 310 CWLPFFHVGRIIYINTEDSR---MMYFSQVFNVALQLFVLSASINPILNLSKKYRAA 365  
 320 CWLPFVHVRRLMFCYISDEQWTFELDFYHYFVMTNALFYVSSAINPILNLSVANFRQV 379

QY 366 AFKLLLA-----RKSRP 377  
 DB 380 FLSTLACLCPGWHRHRRKRP 399

RESULT 7  
 NTRL\_MOUSE  
 ID NTRL\_MOUSE STANDARD; PRT; 424 AA.  
 AC 088319;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Neurotensin receptor type 1 (NT-R-1).  
 GN NTSR1 OR NTSR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Snider J., Sano H., Ohta M.;  
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Receptor for the tridecapeptide neurotensin. It is  
 associated with G proteins that activate a phosphatidylinositol-  
 calcium second messenger system.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC Highest to tachykinins receptors.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; AB017027; BAA33013.1; -  
 DR MGD; MGI:97386; Ntsr.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR InterPro; IPR003985; NT1\_Receptor.  
 DR InterPro; IPR003984; NT1\_Receptor.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODOPSN.  
 DR PRINTS; PR01479; NEUROTENSINR.  
 DR PRINTS; PR01480; NEUROTENSINR.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Phosphorylation; Lipoprotein; Palmitate.  
 FT DOMAIN 1 64  
 FT TRANSMEM 65 87  
 FT DOMAIN 88 96  
 FT CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 97 121  
 FT DOMAIN 122 143  
 FT TRANSMEM 144 165  
 FT DOMAIN 166 188  
 FT TRANSMEM 189 210  
 FT DOMAIN 211 235  
 FT TRANSMEM 236 260  
 FT DOMAIN 261 308  
 FT TRANSMEM 309 330  
 FT DOMAIN 331 348  
 FT TRANSMEM 349 372  
 FT DOMAIN 373 424  
 FT CYTOPLASMIC (POTENTIAL).  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 38 38  
 FT CARBOHYD 42 42  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT DISULFID 211 224  
 FT BY SIMILARITY.

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FT LIPID 388 388 S-palmitoyl cysteine (Potential).
SQ SEQUENCE 424 AA; 47216 MW; 8E9A723171A48711 CRC64;

Query Match 23.08; Score 495.5; DB 1; Length 424;
Best Local Similarity 33.6%; Pred. No. 6.6e-26;
Matches 127; Conservative 56; Mismatches 114; Indels 81; Gaps 12;

QY 39 PVPTAVCLCFVVGVSNGVVTVMILGR---YDRMRTTNNLYLGSMAVSDLLI-LLGLPFD 94
Dd 64 VLVTAVYALFVVGTVGNSVTAFTLARKKSLQSIQSVHYHGLSLALSDLLILLAMPE 123
QY 95 LYR-LWRSRWVFGPLICRLSLYVCEGCTATLHNTALSVERYLATCRPLRARVLTTR 153
Dd 124 LYNFIFWHHPWAFGDAGCRGYFURDACTATALNVASLSVRYLATCHPFAKTLMSRS 183
QY 154 RVRALIAVLMAVALLSAGPFLFVGVQDPCGISVVPGLNGTARTASSPLASSPPLMLSRA 213
Dd 184 RTKFIISAIWLASALLAVPMLFTWGLQ-----NRS 213
QY 214 PPPSPGPGPETAEEAALFSRECPSPALQALRVMLVWTTAYFL-PPLCLSLILYGLIGR 272
Dd 214 ADGQHPGG-----LVCTPT-VDTATVKVVIQVNTFMSFLFPMLIISILNTVIAN 261
QY 273 EL-----KSSRPLRGPASGR-----ERGHROTQR-----VLAIVVLAFLICW 311
Dd 262 KLTVMVHQABQGRGVCTVGTHTNSLEHSTFNMSIEPGRVQALRHGVLRVLAIVVAVVVCW 321
QY 312 LPFHVGRIIYINTDSR-----MMVFQSVFNIVALQLFYLASINPILYMLSKKYRAAF 367
Dd 322 LPYHVRIMFCYISDEQWTTFLDFYHYFYMVLTALFVSSAIPILYNLVNANFRQVFL 381
QY 368 KLLLA-----RKSRP 377
Dd 382 STLACLCPGWRRRRKKRP 399

RESULT 8
NTRI HUMAN STANDARD; PRT; 418 AA.
AC P30989; Q9H4H1; Q9H4T5;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neurotensin receptor type 1 (NT-R-1) (High-affinity levo-cabastine-
DE insensitive neurotensin receptor) (NTRH).
GN NTR1 OR NTRR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93154505; PubMed=8381365;
RA Vita N., Laurent P., Lefort S., Chalou P., Dumont X., Kaghad M.,
RA Gully D., le Fur G., Ferrara S., Caput D.;
RT "Cloning and expression of a complementary DNA encoding a high
RT affinity human neurotensin receptor.";
RL FEBS Lett. 317:139-142(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blake S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhumi P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grahm D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
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RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leivaesalho M.H., Leverha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McIlroy K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RA "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -!- FUNCTION: Receptor for the tridecapeptide neurotensin. It is
CC associated with G proteins that activate a phosphatidylinositol-
CC calcium second messenger system.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC Highest to tachykinins receptors.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X70070; CAA49675.1; -
CC EMBL; AL357033; CAC14923.1; -
CC EMBL; AL035669; CAC12747.1; -
CC PIR; S29506; S29506.
CC HSSP; P02699; 1F88.
CC Genew; HGNC:8039; NTSR1.
CC MIM; 162651; -
CC GO; GO:0005783; C:endoplasmic reticulum; TAS.
CC GO; GO:0005794; C:Golgi apparatus; TAS.
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0004930; P:G-protein coupled receptor activity; TAS.
CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.
CC GO; GO:0007268; P:synaptic transmission; TAS.
CC InterPro; IPR000276; GPCR_Rhodops.
CC InterPro; IPR003985; NTL_receptor.
CC InterPro; IPR003984; NT_receptor.
CC Pfam; PF00001; 7tm1; 1.
CC PRINTS; PR00237; GPCRHOODPSN.
CC PRINTS; PR01479; NEUROTENSINR.
CC PRINTS; PR01480; NEUROTENSINR.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS02622; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 63
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 64 86
FT DOMAIN 87 95
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 120
FT DOMAIN 121 142
FT DOMAIN 143 164
FT TRANSMEM 165 187
FT DOMAIN 188 209
FT TRANSMEM 210 234
FT DOMAIN 235 259
FT TRANSMEM 260 303
FT TRANSMEM 304 325
FT DOMAIN 326 343
FT TRANSMEM 344 367
FT DOMAIN 368 418
FT CARBOHYD 4
FT CARBOHYD 37
FT CARBOHYD 41
FT DISULFID 141
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT BY SIMILARITY.
FT 224
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DR EMBL; AF522193; AAN10046.1; -
DR EMBL; AF505865; AAO20968.1; -
DR EMBL; AE003594; AAF51746.2; ALT_SEQ.
DR FlyBase; FBgn0037100; capar.
DR GO; GO:0016021; C: integral to membrane; NAS.
DR GO; GO:0004930; F: G-protein coupled receptor activity; IDA.
DR GO; GO:0008188; F: neuropeptide receptor activity; IDA.
DR GO; GO:0007589; P: fluid secretion; TAS.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor; G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 72 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 73 93 1 (POTENTIAL).
FT DOMAIN 94 109 2 (POTENTIAL).
FT TRANSMEM 110 130 3 (POTENTIAL).
FT DOMAIN 131 145 4 (POTENTIAL).
FT TRANSMEM 146 165 5 (POTENTIAL).
FT DOMAIN 167 189 6 (POTENTIAL).
FT TRANSMEM 190 210 7 (POTENTIAL).
FT DOMAIN 211 237 8 (POTENTIAL).
FT TRANSMEM 238 258 9 (POTENTIAL).
FT DOMAIN 259 295 10 (POTENTIAL).
FT TRANSMEM 296 316 11 (POTENTIAL).
FT DOMAIN 317 335 12 (POTENTIAL).
FT TRANSMEM 336 356 13 (POTENTIAL).
FT DOMAIN 357 477 14 (POTENTIAL).
FT DISULFID 142 228 BY SIMILARITY.
FT CARBOHYD 2 2 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 13 13 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SEQUENCE 477 AA; 54004 MW; 34FBE13F301A9FAD CRC64;

Query Match
Best Local Similarity 29.7%; Score 451; DB 1; Length 477;
Matches 117; Conservative 69; Mismatches 135; Indels 74; Gaps 11;

QY 8 SDGPEGAREPPWALPPCDERRCSP-----FPLGALVPVAVCLFLFVVGVSG 55
Db 30 SDPSHGFBEDY----ACGTFNCSPKEFVAFVLGPQPLPYKAVLITIFGGIFITGVWG 85
QY 56 NVVTVMIGRYDMRTTNNLYLGSMVSDLLILL-GLPFDLYLWRSRPMVFGPLCLRLS 114
Db 86 NLLVCVILIRHSAMHTATNYLFSLAVSDLLYLLGLPFEVLYWQYPLFGWPFCKIR 145
QY 115 LVYGECTVATLHMTALSVERVLAICRPARAVLVTRRRVRLAIVLMAVALLSAGPFL 174
Db 146 AFISEACTYVSPTIVAFSGMERELAICHPLHLVYAMVGFKRAIRITALTMTVTSFSAIPF- 204
QY 175 FLVGVQDPGISVVVGLNGTARIASSPLPWLWRAPPPSPGPTAEAAALFSRE 234
Db 205 -----GLLSDIQVNLPLDHS-----RIESAF----- 227
QY 235 CRPSPAQLGALRYMLVWTVTAYFFLPFLCLISLYGLICRELWSSRRPLRG--PAASGRERG 292
Db 228 CSMSPKIVNEIPVFEVSFCIFFVPIPMILLIILLYGRNGAKIRSTNQKLGVOQTNRETR 287
QY 293 HQQTK-----RVLVVVLAFIICWLPFHVGRITTYINTESRMVYFQYENI-----VAL 341
Db 288 NSQMRKKTIVIRMLAAVVITFFVCVFFPHLQRLFLYAKN-----MDNYLDINEALFSIAG 342
QY 342 QLFYLSANIPILYNLISKYRAAFAKLLIARKS 375
Db 343 FAYVSVCTNPVIVSVMSRRYR-VARELLCGKA 375

RESULT 10
ID NTR2 HUMAN STANDARD; PRT; 410 AA.
AC Q95655; Q8TBH6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neurotensin receptor type 2 (NT-R-2) (Levocabastine-sensitive
DE Neurotensin receptor) (NTR2 receptor).
GN NTR2.
OS Homo sapiens (Human).
OC Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99086919; PubMed=9851594;
RA Vita N., Oury-Donat F., Chalon P., Guillemot M., Kaghad M., Bachy A.,
RA Thurneyssen S., Garcia S., Poinot-Chazel C., Casellas P., Keane P.,
RA Le Fur G., Maffrand J.-P., Shoubrie P., Caput D., Ferrara P.,
RT "Neurotensin is an antagonist of the human neurotensin NT2 receptor
RT expressed in Chinese hamster ovary cells.";
RL Eur. J. Pharmacol. 360:265-272(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max A.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez Y., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Receptor for the tridecapeptide neurotensin. It is
CC associated with G proteins that activate a phosphatidylinositol-
CC calcium second messenger system.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC Highest to tachykinins receptors.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; Y10148; CAA71233.1; -
CC EMBL; BC022501; AAB22501.1; -
CC GenBank; HGNC:8040; NTR2.
CC MIM; 605538; -
CC GO; GO:0005887; C: integral to plasma membrane; TAS.
CC GO; GO:0004930; F: G-protein coupled receptor activity; TAS.
CC GO; GO:0007166; P: cell surface receptor linked signal transdu. .; TAS.
CC GO; GO:0007600; P: sensory perception; TAS.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC InterPro; IPR003986; NT2_receptor.
CC InterPro; IPR003984; NT_receptor.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PRINTS; PR01479; NEUROTENSINR.
CC PRINTS; PR01481; NEUROTENSINR.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

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```
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Lipoprotein; Palmitate.
FT DOMAIN 1 32
FT TRANSMEM 33 55
FT DOMAIN 56 64
FT TRANSMEM 65 87
FT DOMAIN 88 109
FT TRANSMEM 110 131
FT DOMAIN 132 154
FT TRANSMEM 155 176
FT DOMAIN 177 217
FT TRANSMEM 218 237
FT DOMAIN 238 298
FT TRANSMEM 299 337
FT DOMAIN 338 358
FT TRANSMEM 359 410
FT DISULFID 108 194
FT LIPID 377 377
FT CONFLICT 168 168
FT CONFLICT 367 367
SQ SEQUENCE 410 AA; 45413 MW; 8C3AD22BE15FD66 CRC64;

Query Match 18.9%; Score 407; DB 1; Length 410;
Best Local Similarity 31.2%; Pred. No. 4.4e-20;
Matches 129; Conservative 60; Mismatches 135; Indels 90; Gaps 16;

QY 17 PPWALPP---CDERRCSFFPLGALVPVTAVCLFVVGSGNVVTVMLI-----GR 65
D 18 PPRPSSNPGSLDARLGVDTTRIMAKVLTALYALWALGAGNALSVHVLKARAGR 67
QY 66 YRDMRTTNLYGSAVSDILL-GLPFDLYR-LWRSRPVWFGPFLCLSLYVGEGETY 123
D 68 LRH-----HVLSDALAGLLLVGVFVSVFVWHPVFGDLGCRGYFVHELQAY 120
QY 124 ATLHMTALSVERYLAIQPLRARVLVTRRRVRLIALVLAVALLSAGPFLFLVG- 179
D 121 ATVLVSAGLSAERCLAVCQPLRARSLLTPRTRWLVALSWAASLGALPMAVIMQKHEL 180
QY 180 -----EQDPSVSVPLNGTARIASS-----PLASPPPL-----WLS 211
D 181 ETADGEPEPASRVCVTVL---VSTALQVFIQNVLVSVFLPLTALTAFLNGVTSHLLALCS 238
QY 212 RAPPSPSPGPEATAEAAALFRCRPSPAQCALRVLWLVTTAVFPFLCLSLYGLIG 271
D 239 QVPSTSTP-GSTPSRLELSEE-----GLLSFIWVKT-----FIQG--G 276
QY 272 RELWSSRRPLRGPAASGRGHRQTRVLLVVVLAFLICWLPFHVGRIIYINTEDSR--- 328
D 277 QVSLVRHKDVR-----RIRLSQSVQVLRVAVVMYVICWLPYHARRLMYCVVPDAWTD 330
QY 329 -MMVFSQYFNIVALQLFVLSASINPLYNLISKYRAAFKLLARKSPRPGFH 381
D 331 PLYNFHYFYVNTLFIYSSAVTPLLNAVSSSFR-----KLFEAVSSLCGEH 380

RESULT 11
NTR2_MOUSE
ID_NTR2_MOUSE STANDARD; PRT; 417 AA.
AC P70310.
DT 01-NOV-1997 (Rel. 35, Created)
DI 01-NOV-1997 (Rel. 35, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neurotensin receptor type 2 (NT-R-2) (Low-affinity leucocastine-
DE sensitive neurotensin receptor) (NTRL).
GN NTR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAUB/c; TISSUE=Brain;
```

QY 190 GLNGTARIASSPLASPPWLWRAP-PPSPSGPETAARAAALSRRCRPPSPAQI-----GAL 245  
Db 180 -----MERADGEPEPAS-----RVCTVLVSRRASSRTFQVKGAGLL 215  
QY 246 RVMLWVTTA-----YFFLPFLC-----LSIL--YGLIGRELWSSRRPL 281  
Db 216 RSPFLWELTAILNGITVNHVLVALSQVPSASAQVNSIPSRLELSEGLLGFITWRKTL 275  
QY 282 RGAASGRGRHQTK-----RVLLVVLAFIICWLPFHVGRIIYINTED-----SRMMY 331  
Db 276 GVOASLVHRKDAQIRSLQHSQAQVLAIVAVVVICWLPYHARLMYCYIPDDGWTDELYD 335  
QY 332 FSOYFNIVALQLFVLSINPILYNLISKYRAAPKLLILARKSRPGRHRS 383  
Db 336 FHYFYVWNTLVFVSSAVTPVLYNAVSSFR-----KLFLESLSLSCGEGRS 383

## RESULT 12

NTR2 RAT STANDARD; PRT; 416 AA.  
AC Q63384;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DE Neurotensin receptor type 2 (NT-R-2) (High-affinity levocabastine-sensitive neurotensin receptor).  
GN NTR2 OR NTR2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Hypothalamus;  
RX MEDLINE=96228041; PubMed=8647296;  
RA Chalon P., Vita N., Kaghad M., Guillemont M., Bonin J.,  
RA Delpech B., le Fur G., Ferrara P., Caput D.;  
RT "Molecular cloning of a levocabastine-sensitive neurotensin binding site";  
RL FEBS Lett. 386:91-94(1996).  
CC -!- FUNCTION: Receptor for the tridecapeptide neurotensin. It is associated with G proteins that activate a phosphatidylinositol-calcium second messenger system.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Abundant in cortex and hypothalamus, and lower levels seen in the heart and intestine.  
CC -!- DEVELOPMENTAL STAGE: Expressed maximally in 7-day-old brain and expression decreases progressively until adulthood (35-day-old brain).  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors. Highest to tachykinins receptors.

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CC -----  
CC EMBL; X97121; CAA65787.1; -;  
CC PIR; S68822; S68822.  
CC InterPro; IPR000276; GPCR\_Rhodop.  
CC InterPro; IPR003986; NT2\_receptor.  
CC InterPro; IPR003984; NT\_receptor.  
CC Pfam; PF00001; 7tm 1; 1.  
CC PRINTS; PR00237; GPCR\_RHOOPSN.  
CC PRINTS; PR01479; NEUROTENSINR.  
CC PRINTS; PR01481; NEUROTENSINR.  
CC PROSITE; PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
CC PROSITE; PS00262; G-PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Transmembrane; Lipoprotein; Palmitate.

FT DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 33 55 1 (POTENTIAL).  
FT DOMAIN 56 64 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 65 87 2 (POTENTIAL).  
FT DOMAIN 88 109 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 110 131 3 (POTENTIAL).  
FT DOMAIN 132 154 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 155 176 4 (POTENTIAL).  
FT DOMAIN 177 216 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 217 237 5 (POTENTIAL).  
FT DOMAIN 238 298 6 (POTENTIAL).  
FT TRANSMEM 299 319 7 (POTENTIAL).  
FT DOMAIN 319 337 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 338 358 3 (POTENTIAL).  
FT DOMAIN 359 416 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 108 194 BY SIMILARITY.  
FT LIPID 377 377 S-palmitoyl cysteine (Potential).  
SQ SEQUENCE 416 AA; 46265 MW; 127FC5F5CB6FE208 CRC64;  
Query Match 18.6%; Score 401; DB 1; Length 416;  
Best Local Similarity 29.4%; Pred. No. 1.1e-19;  
Matches 122; Conservative 68; Mismatches 145; Indels 80; Gaps 13;  
QY 18 PWPALP-----PCDERRCSPTPLGALVPVTAACLCLFVVGSGNVVTVMLIGRYDMRT 71  
Db 6 PWPSPSPSAGLSLEARLGVDTRLWAKVLTALYSLIFAFGTAGNALSVHVLKARAGRP 65  
QY 72 -TTNLYGSMVSDLLILL-GLPFDLYR-LWRSRPWVFGPGLLCRLSLVYVGGCTVATLLH 128  
Db 66 GLRYHVLSLALSALLLVNPMELYNFVMSHPWVFGDLGCRGYVYFRELCAVATVLS 125  
QY 129 MTALSVERVLAICRPLRARVLTTRRRVRAIVLVAVALLSAGPFLFLVGV----- 179  
Db 126 VASLSAERCLAVCQPLRARLTPTRTRELLSLVWVASLGLALPMAVINGQKHEVESADG 185  
QY 180 EODPGISVVGPLNGTARIA-----SSPLASSPPLWLSRAPPPSPSPSPETAAR 228  
Db 186 EEPASRVCTVLSRATLVQVFNVLVSFAUPLATAFL-----NGITVNHLM 234  
QY 229 ALFSRECRPSAQLGALRVMLVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPASG 288  
Db 235 ALYS-QVPSASQVSSIPSRLELSE-----EGLLGFTWRKTLISGVQASLV 281  
QY 289 REGRHQTK-----RVLLVVLAFIICWLPFHVGRIIYINTED-----SRMYFSQYFNI 338  
Db 282 RHKDAQIRSLQHSQAQVLAIVAVVVICWLPYHARLMYCYIPDDGWTNELYDFHYFYM 341  
QY 339 VALQLFYLASINPILYNLISKYRAAPKLLILARKSRPGRHRSRPTDAGEVAGD 393  
Db 342 VTNTLFYVSSAVTPILYNVSSFR-----KLF-----ESLGSLSGGE 379

## RESULT 13

SSR5 MOUSE STANDARD; PRT; 362 AA.  
ID SSR5 MOUSE  
AC Q08958; Q08998;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Somatostatin receptor type 5 (SSSR).  
SSR5 OR SMSTR5.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvJ; TISSUE=Liver;  
RX MEDLINE=97444289; PubMed=9300821;  
RA Lublin A.L., Diehl N.L., Hochgeschwender U.;  
RT "Isolation and characterization of the gene encoding the type 5 mouse (Mus musculus) somatostatin receptor (msst5).";  
RT Gene 195:63-66(1997).  
RL





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DR EMBL; X74828; CAA52825.1; -.
DR PIR; I57940; I57940.
DR HSP; P02699; I588.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G PROTEIN RECF F1.1; 1.
DR PROSITE; PS0262; G PROTEIN RECF F1.2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Lipoprotein; Palmitate.
FT DOMAIN 1 35 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 36 63 1 (POTENTIAL).
FT DOMAIN 64 73 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 74 99 2 (POTENTIAL).
FT DOMAIN 100 111 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 112 133 3 (POTENTIAL).
FT DOMAIN 134 155 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 156 176 4 (POTENTIAL).
FT DOMAIN 177 196 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 197 221 5 (POTENTIAL).
FT DOMAIN 222 247 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 248 273 6 (POTENTIAL).
FT DOMAIN 274 283 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 284 308 7 (POTENTIAL).
FT DOMAIN 309 363 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 13 13 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 23 23 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 110 185 BY SIMILARITY.
FT LIPID 320 320 S-Palmitoyl cysteine (Potential).
SQ SEQUENCE 363 AA; 39971 MW; 48D4512960613B4A CRC64;

Query Match
Best Local Similarity 16.6%; Score 358; DB 1; Length 363;
Matches 110; Conservative 27.3%; Pred. No. 6.6e-17; Indels 84; Gaps 12;

QY 5 WNGSDGEGAREPPWPALPPCDERRCSPPFLGA---LVPVTAVCLCLFVVGVSGNVVTVM 61
Db 12 WNASASGNGHN--WSLVG-----SASPMGARAVLPVLYLLVC--TVGLSGNTLIVY 60

QY 62 LIGRYDRMRTTNLYLGMAVSLLILLGLPDLRLWRSPWFGPLLCRLSLYVGE 121
Db 61 VLIRHAKMTVTNVYTLNLAADVLFMLGLPFLATQNAVVSYPFGSFLCRLVMTLDGIN 120

QY 122 TYATLLHMTALSVERYLAI CRPLRARVLVTRVRRIALIVLMAVALISAGPFLVGVQE 181
Db 121 QFTSIFCLMWSVDRLAVVHPLRSARWRPRVAKASAAVWVFLMSLPLLVFADVQE 180

QY 182 DPGISVVGUNGRTARIASSPLASPPPLWLSRAPPPSPGPETAATAAALFSRECRPSPAQ 241
Db 181 G-----WGTCNLS-----W-----PEPVG 194

QY 242 LGLALRVMLVTTAYFELPFLCISILYGLI-----GRELWSSRRPLRGPAAGRGRHR 294
Db 195 LMGAAFTVSVLGGFGLLVICLVLLIVVKAAGMRVGSRR-----RRRSEP 244

QY 295 QTRKVLVVVLAFTICWLPVHGRIIYN-TEDSRMMYFQYENIVALQLFVLSASINPI 353
Db 245 KVTMRVVVVVLFVGCWLPFFIVNVNLAFTLPEETSAGLYFVVVLS--YANSCANPL 302

QY 354 LYNLSKKYRAAFKULLARKSPRGHRSRDRTAGEVAGDTG 396
Db 303 LYGLFLSDNFRQSPKVLCLR---RGYGMEDADAIEPRPDKSG 341

RESULT 15
SSR3_HUMAN
ID SSR3_HUMAN STANDARD; PRT; 418 AA.
AC P32745;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Somatostatin receptor type 3 (SS3R) (SSR-28).

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GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93149123; PubMed=1337145;
RA Yamada Y., Reisine T., Law S.F., Ihara Y., Kubota A., Kagimoto S.,
RA Seino M., Seino Y., Bell G.I., Seino S.;
RT "Somatostatin receptors, an expanding gene family: cloning and
RT functional characterization of human SS3R, a protein coupled to
RT adenylyl cyclase.";
RL Mol. Endocrinol. 6:2136-2142(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93238970; PubMed=8097479;
RA Connors J.D., Demchishyn L.L., Seeman P., van Tol H.H.M.,
RA Strikant C.B., Kent G., Patel Y.C., Niznik H.B.;
RT "A human somatostatin receptor (SS3R), located on chromosome 22,
RT displays preferential affinity for somatostatin-14 like peptides.";
RL FEBS Lett. 321:279-284(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX Kopatz S.A., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057165; PubMed=10591208;
RA Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Baggeley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgman A.M., Buck D., Burgess J.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kubasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuura S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Mala J.E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing J.,
RA Scheet P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson T.,
RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
RA Feyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
RA O'Brien K.P., Wilkinson P., Bodenreich A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tilahun Y., Wright H.;
RT "The DNA sequence of human chromosome 22.";

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RL Nature 402:489-495(1999).
CC -!- FUNCTION: Receptor for somatostatins-14 and -28. This receptor is
CC coupled via pertussis toxin sensitive G proteins to inhibition of
CC adenylyl cyclase.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Brain, pituitary and pancreas.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M96738; AA860592.1; -.
CC EMBL; Z82188; CA845263.1; -.
CC EMBL; AY322541; RAP84354.1; -.
CC PIR; A46226; A46226.
CC HSP; P34996; 1DDO.
CC Genew; HGNC:11332; SSTR3.
CC MIM; 182453; -.
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:004994; P:somatostatin receptor activity; TAS.
CC GO; GO:0007267; P:cell-cell signaling; TAS.
CC GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. . .; TAS.
CC GO; GO:0008628; P:induction of apoptosis by hormones; TAS.
CC GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm1; 1.
CC PRINTS; PR00237; GPCRRHODOPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Multigene family; Polymorphism
KW DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 44 69 1 (POTENTIAL).
FT DOMAIN 70 79 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 80 101 2 (POTENTIAL).
FT DOMAIN 102 116 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 117 138 3 (POTENTIAL).
FT DOMAIN 139 161 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 162 181 4 (POTENTIAL).
FT DOMAIN 182 205 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 206 231 5 (POTENTIAL).
FT DOMAIN 232 257 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 258 279 6 (POTENTIAL).
FT DOMAIN 280 293 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 294 316 7 (POTENTIAL).
FT DOMAIN 317 418 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 17 17 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 30 30 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 116 191 BY SIMILARITY.
FT DOMAIN 346 360 GLU-RICH (ACIDIC).
FT VARIANT 411 411 S-> T (in dbSNP:229568).
FT /FTID=VAR_011853.
SQ SEQUENCE 418 AA; 45847 MW; 1227095F801190C4 CRC64;

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Query Match 16.5%; Score 356.5; DB 1; Length 418;  
Best Local Similarity 26.9%; Pred. No. 9,5e-17;  
Matches 101; Conservative 63; Mismatches 146; Indels 65; Gaps 10;

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QY 11 PEGAREPFWPALPPCDERCSPFPL-----GALVPTAVCLCLFVYGVSGNVVTVMLIGR 65
DQ ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DQ 15 PENA--SSAPPDATTGNVSGAPSPAGLAVSGVLIPLVYVVC--VVGGLGNSLVIYVVL 71
QY 66 YRDMETTNLYGSMVADLLILGLPEOLYLRWSRPWVFGPLLCRLSLYVGECTVAT 125
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ 72 HTASPSVTNVILNALADELFMLGLPF-LAAQNALSYWPFGLMCRLVNAVVDGINQFTS 130
QY 126 LLHMTALSVERYLAICRPLRARVLVTRRRVRALLAVLWAVALLSAGPFLFLVGVQDDPGI 185
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db 131 IPCLTMSVDRLAVVHETRSARWETAPVARTVSAVWVAVVVLPVTVFSGV----- 184
QY 186 SVVPLGNGTARIASSPLASSPPLMLSRAPPSPGPGPTAATAAALFSRECR---PSPAQL 242
Db 185 -----PRGMST-----CHMQWPEPAAA 201
QY 243 GALRVMLVWTTAYFPLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGREGHROTKEVLLV 302
Db 202 WRAGFIITTAALGFPGPLLVICLYLLVVKRAGRRVWAPSCORRRSRRRVTRMVVA 261
QY 303 VYLAFTICWLPFHVGRITTYINTE-DSRMMYFSQYFNIVALQVLYLSASINPILYNLSKK 361
Db 262 VVALFVLCWMPFYVLNIWVVCPLPEEPAFGLYFLVALP--YANSCANPILYGFLSYR 319
QY 362 YRAAFKLLLLARKSR 376
Db 320 FK-QGFRVLLRPSR 333

```

Search completed: July 4, 2004, 03:07:50  
Job time : 20 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 4, 2004, 02:04:17 ; Search time 73 Seconds  
(without alignments)  
1780.733 Million cell updates/sec

Title: US-09-876-252-130  
Perfect score: 2156  
Sequence: 1 MGSPWNGSDPEGAREPPWP.....DTGSDTVGYTETSANVKTMG 412

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	901	41.8	363	13	Q93413 spherooides
2	855.5	39.7	364	11	Q8BWX8 mus musculus
3	849	39.4	347	13	Q7ZT14 gallus gall
4	845	39.2	374	13	Q93412 spherooides
5	819.5	38.0	366	6	Q8MH25 ovis aries
6	753	34.9	331	13	Q7ZZJ9 gallus gall
7	637	29.5	267	13	Q7ZZJ8 gallus gall
8	602	27.9	559	13	Q93414 spherooides
9	486.5	22.6	426	4	Q8NE20 spherooides
10	484.5	22.5	426	4	Q8NE20 spherooides
11	475.5	22.1	395	11	Q91276 mus musculus
12	475.5	22.1	395	11	Q8BZ39 mus musculus
13	475	22.0	415	4	Q96AM5 mus musculus
14	474	22.0	415	4	Q9GZ04 mus musculus
15	472.5	21.9	395	11	Q9J1B1 mus musculus
16	470.5	21.8	395	11	Q9ESQ4 mus musculus

17	456.5	21.2	405	11	O55040
18	434	20.1	418	5	O17239 caenorhabdi
19	430	19.9	428	5	Q9VFN4 drosophila
20	430	19.9	430	5	Q8ITC9 drosophila
21	414	19.2	595	5	Q8ITD0 drosophila
22	414	19.2	593	5	Q9VFW6 drosophila
23	410	19.0	402	11	Q9J1B2 mus musculus
24	405	18.8	412	11	Q9J1J5 rattus norv
25	396.5	18.4	416	11	Q8VIF5 mus musculus
26	395.5	18.3	416	11	Q920Q5 mus musculus
27	386	17.9	660	5	Q9VFW5 drosophila
28	384	17.8	658	5	Q8ITD1 drosophila
29	378	17.5	378	5	Q18701 caenorhabdi
30	376	17.4	123	11	Q80UB2 mus musculus
31	370.5	17.2	461	5	Q86RK9 drosophila
32	369.5	17.1	385	11	Q9JK40 mus musculus
33	368.5	17.1	461	5	Q86C62 drosophila
34	368.5	17.1	471	5	Q86RL0 drosophila
35	368.5	17.1	471	5	Q86C63 drosophila
36	357.5	16.6	377	13	Q7T2S9 carassius a
37	356.5	16.5	385	4	Q86VF2 homo sapien
38	356	16.5	452	13	Q7T2S8 carassius a
39	355.5	16.5	401	13	Q8JFZ6 xenopus lae
40	353.5	16.4	401	13	Q9DDR0 xenopus lae
41	349	16.2	477	13	Q8JIDS carassius a
42	348.5	16.2	367	6	Q8MI04 ovis aries
43	344	16.0	440	13	Q7T298 brachydanio
44	340.5	15.8	370	13	Q8UWLS fugu rubrip
45	339	15.7	145	6	O97914 ovis aries

## ALIGNMENTS

## RESULT 1

O93413 ID O93413 PRELIMINARY; PRT; 363 AA.  
AC O93413  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Orphan G protein-coupled receptor.  
OS Spherooides nephelus  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Spherooides.  
OX NCBI\_TaxID=39110;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=2002336; PubMed=10628755;  
RA Palyha O.C., Feighner S.D., Tan C.P., McKee K.K., Hreniuk D.L.,  
RA Gao Y.D., Schleim K.D., Yang L., Morriello G.J., Nargund R.,  
RA Patchett A.A., Howard A.D., Smith R.G.  
RT "Ligand activation domain of human orphan growth hormone (GH)  
secretagogue receptor (GHS-R) conserved from pufferfish to humans.";  
RL Mol. Endocrinol. 14:160-169(2000).  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL; AF082210; AAC33473.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm 1; 1.  
DR PRINTS; PR00237; GPCRHHODPSN.  
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.  
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL2; 1.  
KW G-protein coupled receptor; Transmembrane.  
SQ SEQUENCE 363 AA; 41324 MW; 74518BD9CD310991 CRC64;  
Query Match 41.8%; Score 901; DB 13; Length 363;



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QY 213 APPSPSPGPTAEEALFSRECRPSAQL--GALRVMLVWTTAYFFLPFLCLSLYLGLI 270
Db 178 -----ECRATEVAIRSGLLTMMVSISSIFFLPVFLVLLVLSLI 216
QY 271 GRELWSSRRPRLGPAASGRGRHQTRKVLVVVLAFTICLWLPFHVGRRIIYINTEDS--- 327
Db 217 GRKLWRRKRKNIGPSTIIDKNNKQTVKMLVVVVVFAFICLWLPFHVGRYLSKSPFAGSL 276
QY 328 RMYFQYFNIVLQOLFYLSSINPILYNLSKKYRAAFAKLLARKSRPR 378
Db 277 EIAVISQCNLVSVFLVFLYSAINPILYNIMSKYRVAACR-LFLGKALPK 326

RESULT 4
O93412 PRELIMINARY; PRT; 374 AA.
ID O93412
AC O93412;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Orphan G protein-coupled receptor.
OS Spherooides naphelus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Spherooides.
OX NCBI_TaxID=39110;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20092336; PubMed=10628755;
RA Palyha O.C., Feighner S.D., Tan C.P., McKee K.K., Hreniuk D.L.,
RA Gao Y.D., Schleim K.D., Yang L., Morriello G.J., Nargund R.,
RA Patchett A.A., Howard A.D., Smith R.G.;
RT "Ligand activation domain of human orphan growth hormone (GH)
RT secretagogue receptor (GHS-R) conserved from pufferfish to humans."
RT Mol. Endocrinol. 14:160-169(2000).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF082209; AAC33472.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR PROSITE; PS00043; HTH_GNTR_FAMILY; 1.
KW G-protein coupled receptor; Transmembrane.
SQ SEQUENCE 374 AA; 42324 MW; 2CF9304F004C7A16 CRC64;

Query Match 39.2%; Score 845; DB 13; Length 374;
Best Local Similarity 45.5%; Pred. No. 1e-62;
Matches 187; Conservative 64; Mismatches 102; Indels 58; Gaps 12;

QY 5 WNGS-DSPEGAREPWPALPCDERRCSFPFGLAVPVTAVCLFVVGSGNVTWMLI 63
Db 13 WEGSHNGTAGLELP-----LNYSIPLAVITACTVLFTVVGSGNVTWMLI 61
QY 64 GRYDMRTTNLYLGSMAVSDLLILLGLFPDLYRLWRSPVWVGPELLCRSLYVGECTY 123
Db 62 SRYDMRTTNLYLGSMAVSDLFIFVCMPLDLYRWRYRPRFGBALCKLQFVSESTY 121
QY 124 ATLLHMTALSVERYLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVGVGEQDP 183
Db 122 STILCITALSVERYLAICFPLRAKALVTKRVRALLILLWTVSLLSAGPFWVGVEKDS 181
QY 184 GISVVPGLNGTARIASSPL-ASSPPLMLSRAPPPSPGPTAEEALFSRECRPS--PA 240
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Db 182 --IMFPN-----SSDLNESSWPL-----EAVDTRECRMTQAV 212
QY 241 QLGAIRVMLWTTAYFFLPFLCLSLYLGLIGRELWSSRRPLR-GPAASGRGRGRHQTRKV 299
Db 213 ESGLMEAMVWSSVFFMPFVCLTVLYGLIGRLWLRHRETTINSRVAYRDKSNRQITKM 272
QY 300 LVVVLAFTICLWLPFHVGRRIIYINTEDS---RMYFQYFNIVLQOLFYLSSINPILYN 356
Db 273 LVVVLAFTICLWLPFHVGRYLRQFRLDAPSLLLSEYCSLVSVFLVFLYSAINPILYN 332
QY 357 LIISKYRAAFAKLLARKSRPRGRDRTAGEVAGDTGGDTGVGTETSAN 407
Db 333 TMSWKIRGAVARLEGVSDSPFQ---RCR-TASTVKMD-----GWTESTVUS 373

RESULT 5
O8MHZ5 PRELIMINARY; PRT; 366 AA.
ID O8MHZ5
AC O8MHZ5;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Ghrelin/growth hormone secretagogue receptor.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=1, 2, and 3; TISSUE=Pituitary;
RA Murata T., Ikegami R., Morita Y., Shinozaki K.;
RA "Sheep Ghrelin/Growth Hormone Secretagogue Receptor."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY093948; AAM19733.1; -.
DR EMBL; AY093949; AAM19734.1; -.
DR EMBL; AY093950; AAM19735.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 366 AA; 41486 MW; 2F276651BC6C5D57 CRC64;

Query Match 38.0%; Score 819.5; DB 6; Length 366;
Best Local Similarity 42.1%; Pred. No. 1.4e-60;
Matches 175; Conservative 62; Mismatches 114; Indels 65; Gaps 8;

QY 5 WNGSDGPE-----GAREPWPALPCD-----ERRCSFPFGLAVPVTAVCLFVVGSGN 56
Db 2 WNAFRSELGNLTLPLDLDWAAPDNDLSLTDELPLFPAPLLAGVTATCVALFVVGAGN 61
QY 57 VTVMLIGRVDMMTTNNLYLGSMAVSDLLILLGLFPDLYRLWRSPVWVGPELLCRSLY 116
Db 62 LLTMLVSVRFELRTTNLYLSSMAFSDLLITFLCMPLDLVRLMHYRPNWLDLCKLQF 121
QY 117 VGECTYATLLHMTALSVERYLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFL 176
Db 122 VSSECTIVLITALSVERYLAICFPLRAKALVTKRVRALLILLWTVSLLSAGPFW 181
QY 177 VGVQDQPGISVVPGLNGTARIASSPLASPLWLSRAPPPSPGPTAEEALFSRECR 236
Db 182 VGVHE-----NCT-----DPRD-----TNECR 199
QY 237 PS--PAQLGALRVMLWTTAYFFLPFLCLSLYLGLIGRELWSSRRPLRGAASGRGRHR 294
Db 200 ATEFAVRSGLLITIMVWVSSITFFFLPVCLTVLYSLIGRLWRRRRSRVWVGASLRDQNHK 259
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Query Match      22.0%; Score 475; DB 4; Length 415;
Best Local Similarity 30.8%; Pred. No. 1.3e-31;
Matches 115; Conservative 78; Mismatches 98; Indels 82; Gaps 12;

QY 30 CSPFPLGALVPVAVCLCLFVVGVSGNVVTVMLIGRYDRMTTNLYLGSMAVSDLLI-L 88
DB 37 CGPRRSHPFLPVSVVYVPIFVVGVVGNVLVCLVILQHQAMKTPNYLFLSLAVSDLLVL 96

QY 89 LGLPDLVLMRSRPNVPGPLICRLSLYVGECTYATLLHMTALSVERYLAIICRLARV 148
DB 97 LGMPLEVMERNYFELFGVPCYKTALETVCFASILSITTVSVERVAILHPFRKL 156

QY 149 LVTRRRVRLIALVMAVALLSAGPFLVGVGE--QDPGISVVPGLNGTARIASSPLASP 206
DB 157 QSTRRRALRILGVWGFVSLPNTSIHGKHFYFNGSLVFG-----YNFIIQVTSFLYLLPMTVISV 208

QY 207 PWLSRAPPPSPGPETAEEAALFSRECRPSPAQIGALRVMLVWTVTAYFF-LPFLCLSI 265
DB 209 PMWI-----YNFIIQVTSFLYLLPMTVISV 234

QY 266 LYGCLIGRELWSSR-----RPLRGPASGRERGHQRTKRVLLVVLAFIICWLP 313
DB 235 LYYMALRLKOKSLEADGNANIQRPCR-----KSVNKMFLVLVLFALICWAP 283

QY 314 FHVGRLLIYNTED-SRMVYFSQVENIVAL---QLFYLSASINPILYNLSKRYAAAFKL 369
DB 284 FHIDRLFFSFEWESES--AAVFNLVHVGVSFFYLSSAVNPIIYNLSRRFQ-AAFQN 340

QY 370 LLAKRSRPRGFR 382
DB 341 VLS-----SPHK 347

RESULT 14
Q9GZQ4 PRELIMINARY; PRT; 415 AA.
AC Q9GZQ4; Q9NRA6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Neuromedin U receptor 2 (Neuromedin U receptor-type 2) (G protein-
DE coupled receptor TGR-1).
GN NMUR2 OR NMUR2R OR TGR-1.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20490668; PubMed=10899166;
RA Raddatz R., Wilson A.E., Artyemyehyn R., Bonini J.A., Borowsky B.,
RA Boteju L.W., Zhou S., Kouranova E.V., Nagorny R., Guevarra M.S.,
RA Dai M., Lerman G.S., Vayase P.J., Brancheck T.A., Gerald C., Forray C.,
RA Adam N.;
RT "Identification and Characterization of Two Neuromedin U Receptors
RT the Centrally Expressed in Peripheral Tissues and the Central Nervous
RT System."
RL J. Biol. Chem. 275:32452-32459 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed=11010960;
RA Shan L., Qiao X., Crona J.H., Behan J., Wang S., Laz T., Bayne M.,
RA Gustafson E.L., Monsma F.J. Jr., Hedrick J.A.;
RT "Identification of a Novel Neuromedin U Receptor Subtype Expressed in
RT the Central Nervous System."
RL J. Biol. Chem. 275:39482-39486 (2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Pang L., Wang S., Laz T., Hedrick J.A.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 4-415 FROM N.A.

```

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MEDLINE=20351041; PubMed=10894543;
RA Howard A.D., Wang R., Pong S.-S., Mellin T.N., Strack A., Guan X.-M.,
RA Zeng Z., Williams D.L., Feighner S.D., Nunes C.N., Murphy B.,
RA Stair J.N., Yu H., Jiang Q., Clements M.K., Tan C.P., McKee K.K.,
RA Hreniuk D.L., McDonald T.P., Lynch K.R., Evans J.F., Auscine C.P.,
RA Caskey T., van der Ploeg L.H.T., Liu Q.;
RT "Identification of receptors for neuromedin U and its role in
RT feeding."
RL Nature 406:70-74 (2000).
RN [5]
RP SEQUENCE OF 4-415 FROM N.A.
RX PubMed=10887190;
RA Hosoya M., Moriya T., Kawamata Y., Ohkubo S., Fujii R., Matsui H.,
RA Shintani Y., Fukusumi S., Habata Y., Hinuma S., Onda H., Nishimura O.,
RA Fujino M.;
RT "Identification and Functional Characterization of a Novel Subtype of
RT Neuromedin U Receptor."
RL J. Biol. Chem. 275:29528-29532 (2000).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF272363; AAG24794.1; -
DR EMBL; AF292402; AAG03064.1; -
DR EMBL; AF242874; AAF82755.1; -
DR EMBL; AB041228; AAF3721.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
DR GO; GO:0001607; F:neuromedin U receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007267; F:cell-cell signaling; TAS.
DR GO; GO:0007417; F:central nervous system development; TAS.
DR GO; GO:0007631; F:feeding behavior; TAS.
DR GO; GO:0007186; F:G-protein coupled receptor protein signaling.; IEA.
DR GO; GO:0007218; F:neuropeptide signaling pathway; TAS.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR005390; NeuromedinU.
DR InterPro; IPR005392; NeuromedinU2.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PRO0237; GPCR_RHODOPSN.
DR PRINTS; PRO1565; NEUROMEDINUR.
DR PRINTS; PRO1567; NEUROMEDINUR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 415 AA; 47725 MW; C2BACD84B313390F CRC64;

Query Match      22.0%; Score 474; DB 4; Length 415;
Best Local Similarity 30.8%; Pred. No. 1.5e-31;
Matches 115; Conservative 78; Mismatches 98; Indels 82; Gaps 12;

QY 30 CSPFPLGALVPVAVCLCLFVVGVSGNVVTVMLIGRYDRMTTNLYLGSMAVSDLLI-L 88
DB 37 CGPRRSHPFLPVSVVYVPIFVVGVVGNVLVCLVILQHQAMKTPNYLFLSLAVSDLLVL 96

QY 89 LGLPDLVLMRSRPNVPGPLICRLSLYVGECTYATLLHMTALSVERYLAIICRLARV 148
DB 97 LGMPLEVMERNYFELFGVPCYKTALETVCFASILSITTVSVERVAILHPFRKL 156

QY 149 LVTRRRVRLIALVMAVALLSAGPFLVGVGE--QDPGISVVPGLNGTARIASSPLASP 206
DB 157 QSTRRRALRILGVWGFVSLPNTSIHGKHFYFNGSLVFG-----YNFIIQVTSFLYLLPMTVISV 208

QY 207 PWLSRAPPPSPGPETAEEAALFSRECRPSPAQIGALRVMLVWTVTAYFF-LPFLCLSI 265
DB 209 PMWI-----YNFIIQVTSFLYLLPMTVISV 234

QY 266 LYGCLIGRELWSSR-----RPLRGPASGRERGHQRTKRVLLVVLAFIICWLP 313
DB 235 LYYMALRLKOKSLEADGNANIQRPCR-----KSVNKMFLVLVLFALICWAP 283

QY 314 FHVGRLLIYNTED-SRMVYFSQVENIVAL---QLFYLSASINPILYNLSKRYAAAFKL 369
DB 284 FHIDRLFFSFEWESES--AAVFNLVHVGVSFFYLSSAVNPIIYNLSRRFQ-AAFQN 340

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QY 370 LLARKSRPRGFR 382  
Db 341 VIS-----SFHK 347

227 LYLMGLRLKROESLEANKVAVNIHRPSKSVTKMLFVLVLVFAICWTPPHVDRLFFSFV 286  
325 ED--SRMMYFSQYFNIVAIQLFYLSASINPILYNLISKKYRAAFAKLLLA-----RKS 375  
287 EEWTESLAAVFNLIHVVSQYFFVYLSAVNPITYNLLSRFR-AAFRNVVSPCKWCHPRH 345  
376 RPRG 379  
346 RPOG 349

Search completed: July 4, 2004, 03:10:21  
Job time : 76 secs

## RESULT 15

Q9JIB1  
ID Q9JIB1 PRELIMINARY; PRT; 395 AA.  
AC Q9JIB1;  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
DE Neuromedin U receptor 2.  
GN NMU2R.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley;  
RX MEDLINE=20351041; PubMed=10894543;  
RA Howard A.D., Wang R., Pong S.-S., Mellin T.N., Strack A., Guan X.-M.,  
Zeng Z., Williams D.L., Feigener S.D., Nunes C.N., Murphy B.,  
Stair J.N., Yu H., Jiang Q., Clements M.K., Tan C.P., McKee K.K.,  
Hreniuk D.L., McDonald T.P., Lynch K.R., Evans J.F., Austin C.P.,  
Caskey T., van der Ploeg L.H.T., Liu Q.;  
RA "Identification of receptors for neuromedin U and its role in  
RT feeding";  
RL Nature 406:70-74 (2000).  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL; AF242875; AAF82756.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0001607; F:neuromedin U receptor activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR InterPro; IPR005390; NeuromedinU.  
DR InterPro; IPR005392; NeuromedinU2.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PRINTS; PR00237; GPCRHOPOSPN.  
DR PRINTS; PR01565; NEUROMEDINUR.  
DR PRINTS; PR01567; NEUROMEDU2R.  
DR PROSITE; PS00237; G\_PROTEIN RECP Fl\_1; 1.  
DR PROSITE; PS0262; G\_PROTEIN RECP Fl\_2; 1.  
KW G-protein coupled receptor; Receptor; Transmembrane.  
SQ SEQUENCE 395 AA; 44722 MW; 01D3765B5D5355C0 CRC64;

Query Match 21.9%; Score 472.5; DB 11; Length 395;  
Best Local Similarity 30.5%; Pred. No. 1.9e-31;  
Matches 111; Conservative 81; Mismatches 115; Indels 57; Gaps 9;

QY 30 CSPFPLGALVPTAVCLCLFVVGSGNVVTVMILIGRYDMETTTNLYLGSMAVSDLLI-L 88  
Db 29 CGPKRSLSLPVSAYALIFLVGNGNLLVCMVIRHQTPTNYLFLSLAVSDLLVLL 88

QY 89 LGLPFDLYRLWRSPWVFGPPLCLRLSLYVGGCTYATLLHMTALSVRYLAICRPLRARV 148  
Db 89 LGMPLEIYEMWNNPFLPGVGYFKTALFETVCVFASILSVTVSVRYVAIVHPFRAKL 148

QY 149 LVTRRRVALLAVLWALLSAGPFLVGV--EQDPGISVVPGLNGTARIASSPLASSP 206  
Db 149 ESTRRRLRIILSLWSFWSFSLPNTSIHGKFKQHPNGSSVPG-----SATCTVTK 200

QY 207 PLWLSRAPPPSPGPETAEEAALFRRCRPSAQLGALRVLWLTWTAYFF-LPFLCLSI 265  
Db 201 PMWV-----YNLIQATSLFLYILPMTLLISV 226

QY 266 LYGLIGRELWSSRRFLRGPASGRGRHQT-KRVLLVVVLAFLICWLPFHVGRIIYINT 324